

GenCore version 5.1.4.p5_4578
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 7, 2003, 15:14:54 ; Search time 134.5 Seconds
(without alignments)
6443.584 Million cell updates/sec

Title: US-09-965-830-1_COPY_6_3257

Perfect score: 6089

Sequence:

1 atgcggccatgcgggcct.....aagaagcacaggggtctga 3252

Scoring table:

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-DB=A_Geneseq_101002 -OFFT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPL-0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=0.0 -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_XLPXY -NO_WMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A_Geneseq_101002:.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5704	93.7	1083	20	AA122426	Human brain specif
2	5698	93.6	1083	21	AA144778	Human Elk voltage
3	5697	93.6	1083	21	AA144779	Human Elk voltage
4	5696	93.5	1083	21	AA144780	Human Elk voltage
5	5695	93.5	1083	21	AA144835	Her94, a potassium
6	5695	93.5	1083	21	AA144835	Her94, a potassium
7	5688	93.4	1080	21	AA177738	Human Elk voltage
8	5675	93.2	1083	21	AA144904	Human ESK1 (hESK1)
9	5649.5	92.8	1082	21	AA144904	Monkey potassium c
10	2529.5	41.5	1107	21	AA144907	Human potassium ch
11	2515	41.3	1102	21	AA144907	Human potassium ch
12	2461.5	40.4	1017	20	AA183028	Rat ESK1 potassium
13	2347	38.5	457	21	AA177739	Human brain specif
14	1901	31.2	1311	22	AB161234	Human ESK1 (hESK1)
15	1832.5	30.1	542	21	AA144905	Drosophila melanog
16	1551	25.5	1159	20	AA132020	Human cation chann
17	1551	25.5	1159	20	AA132020	Human potassium a
18	1551	25.5	1159	22	AA170939	Human eag-related
19	1551	25.5	1159	23	AA199167	Human ether-a-go-g
20	1550	25.5	1159	21	AA185406	Long QT syndrome a
21	1533.5	25.2	1163	21	AA183031	Rat Erg1 potassium
22	1482	24.3	958	23	AA144906	Human potassium ch
23	1473.5	24.2	958	23	AA144906	Human transporter
24	1408.5	23.1	1196	23	AA141189	Human transporter
25	1387	22.8	1174	22	AB165304	Drosophila melanog
26	1369	22.5	962	21	AA183032	Rat Eag1 potassium
27	1369	22.5	962	21	AA149944	Human potassium lo
28	1358.5	22.3	989	21	AA149945	Human potassium lo
29	1355	22.3	905	23	AA161678	Human transporter
30	1334	21.9	988	23	AA14214	Human transporter
31	1332.5	21.9	988	22	AA131714	A human alpha-subu
32	1332.5	21.9	988	23	AB176165	Human potassium ch
33	1331	21.9	988	22	AA101043	Human ether a gogo
34	1120.5	18.4	888	20	AA17399	Human erg subfam1
35	1046	17.2	855	22	AB159695	Drosophila melanog
36	817.5	13.4	626	20	AA17398	Human erg subfam1
37	792	13.0	154	21	AA183029	Rat Elk2 potassium
38	655.5	10.8	377	22	AA193690	Human polypeptide,
39	568.5	9.3	1245	22	AB111953	Human cation chann
40	566	9.3	1203	22	AB184662	Human HCM4 protein
41	566	9.3	1203	23	AA184667	Human hyperpolaris
42	554	9.1	423	22	AB111224	Human K channel ho
43	550	9.0	142	22	AA199662	Human excretory re
44	550	9.0	142	22	AA142477	Human kidney relat

ALIGNMENTS

RESULT 1

AA122426

ID AA122426 standard; Protein; 1083 AA.

XX AA122426;

AC AA122426;

XX 28-SEP-1999 (first entry)

DT Human brain specific potassium channel protein sequence.

DE Human brain specific potassium channel protein sequence.

XX Brain specific potassium channel; human; central nervous system disorder;

KW dementia; cerebral ischaemic sclerosis; therapy.

XX Homo sapiens.

XX WO9937677-A1.

XX PD.

XX 29-JUL-1999.

Thu May 8 08:49:37 2003

PF 20-JAN-1999; 99WO-JP00190.
 XX 04-DEC-1998; 98JP-0346198.
 PR 23-JAN-1998; 98JP-0011434.
 XX (YAMA) YAMANOUCHI PHARM CO LTD.
 PA Miyake A, Mochizuki S, Yokoi H;
 XX WPI: 1999-458683/38.
 DR N-PSDB; AAX84910.
 XX Potassium channel protein expressed specifically in brain tissue and
 PT method for its production
 PS Claim 1; Page 33-39; 63pp; English.
 XX This sequence is the potassium channel protein of the invention,
 CC that is expressed specifically in brain tissue. The protein is used to
 CC treat and investigate disorders of the central nervous system such as
 CC dementia and cerebral ischaemic sclerosis.
 XX SQ Sequence 1083 AA;
 Alignment Scores: Length: 1083
 Pred. No.: 0
 Score: 5704.00 Matches: 1083
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.68% Indels: 0
 DB: 20 Gaps: 0
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 DB 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
 QY 61 CGCTTCGACGCGCAGCAGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 DB 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40
 QY 121 CGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
 QY 181 ATGACGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80
 QY 241 CAACAGATCCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuLeuTyr 100
 QY 301 CGGAAGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120
 QY 361 GGGAGGTGGCT 420
 DB 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140
 QY 421 GGGCCGACAGATGAAGGACAGAGTGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
 DB 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgGlyGlyArgGlyGlyArgGlySer 160
 QY 481 AAAGCTTCAATGCCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
 DB 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
 QY 541 CTGCAAGACGACCCCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
 DB 181 LeuGlnLysGlnProLysGlyLysHisLysLysLysLysLysLysLysLysLysLysPro 200

QY 601 AACTTGCTGAGTACAAAGTAGCCGATCGGAAAGTCGCCCTCATCTCTGTTGCTACTGT 660
 DB 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220
 QY 661 GGGGCACTGAGACACCTGGATGGCTTCATCTGCTGCCACACACTCTATGTATGGTGTCT 720
 DB 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
 QY 721 ACTGTGCCCTACAGCGT 780
 DB 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
 QY 781 CCCAGCGT 840
 DB 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280
 QY 841 CGTACCACATTCGT 900
 DB 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300
 QY 901 CACTACGTCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 DB 301 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320
 QY 961 CATGCTTCAAGGTCAACGT 1020
 DB 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340
 QY 1021 CGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 DB 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360
 QY 1081 ACAGTGTCTATGCGCGT 1140
 DB 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380
 QY 1141 ATGGCGCAGCGGAGATCGAGACGAGCAATCCGAGCTGCTGAGATGGCTGGCTGCAG 1200
 DB 381 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400
 QY 1201 GAGCTGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
 DB 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420
 QY 1261 AACAGCTTCGCGCAGAGTGACACTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1320
 DB 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu 440
 QY 1321 GAGTGTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
 DB 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460
 QY 1381 AGCAGCTCACCACGCGGGCTTCGCAAGCTGTGCTGCCCAACACGACGACGACGACGAC 1440
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 DB 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 500
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 DB 501 ThrAlaIleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgAsp 520
 QY 1561 CTGCGGAGTACATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCC 1620
 DB 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLysGlnArgMetLeuGlu 540
 QY 1621 TACTTCCAGGCGCGCTGCGGTGAACATGTCATCGACCCAGCGAGCTGTGTGAGAGC 1680
 DB 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuGlnSer 560

QY 1681 CTCCCTGACGAGTGGCGCAGACATCGCATCGACCTGCACAAAGGAGGTCTCTGACGCTG 1740
 Db 561 LeuProAspLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580
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 Db 581 ProLeuPheGluAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600
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 Db 601 AlaPheCysThrProGlyGluTyrlleuIleHisGlnGlyAspAlaLeuGlnAlaLeuTy 620
 QY 1861 TTTGCTGCTCTGCTGCTCATGAGGTGCTCAAGGGTGGCACCCTGCTCGCCATCTAGGG 1920
 Db 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleuGly 640
 QY 1921 AAGGCGACCTGATCGGCTGTGAGTGGCGCGCGGAGGAGGTGGTAAAGGCCCAATGCC 1980
 Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgGluGlnValValLysAlaAsnAla 660
 QY 1981 GACGTGAAGGGGCTGACGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
 Db 661 AspValLysGlyLeuThrTyrcysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680
 QY 2041 AGCTTGGCTGTACCCCGAGTTTCCCGCGCTTACGTCTGCTGCTGCTGCTGCTGCTGCT 2100
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 Db 701 SerTyrlleuGlnGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720
 QY 2161 GACAAATACCTTATGTCACGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2220
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 Db 861 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 880
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 QY 2761 GCATCGGGAGAGGCGCGTCCCGCAGCCAGCCACCTCCCGGCTTCTGACAGCCTCTGTGTG 2820

Db 921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 940
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 Db 941 AspThrGlyAlaSerSerTyrcysLeuGlnProProAlaGlySerValLeuSerGlyThr 960
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 Db 961 TrpProHisProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProPro 980
 QY 2941 GCGTCTCAGAGTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
 Db 981 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000
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 QY 3061 TCTGAGGAAGGGCTAGGACTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3120
 Db 1021 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 1040
 QY 3121 ACTGAGAGCGCCCGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
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 QY 3181 GAGATGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
 Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnThrGlnGluGluGly 1080
 QY 3241 ACAGGGTCT 3249
 Db 1081 ThrGlyVal 1083

RESULT 2

AY44778
 ID AY44778 standard; Protein; 1083 AA.

XX AY44778;

XX AC

XX DT 04-MAY-2000 (first entry)

XX DE Human Elk voltage gated potassium channel subunit monomer.

XX DE Voltage gated potassium channel subunit; VGPCs; helix; human; stroke;

XX KW Kv superfamily; Eag family; ether a go-go; Elk subfamily; modulator;

XX KW chromosome 12q13; resting potential; cell excitability; seizure;

XX KW CNS; migraine; psychotic; anticonvulsant; neuroprotective;

XX KW ion flux disorder; reporter molecule; detection; gene therapy;

XX KW antileptin; cerebroprotective; antipsychotic.

XX OS Homo sapiens.

XX FH Key

XX FT Region 452..514 Location/Qualifiers

XX FT /label= P-S6_region

XX FT /note= "Pore-S6 region with conserved amino acids"

XX FT Region 452..710

XX FT /label= Extended P-S6_region

XX FT /note= "Extended Pore-S6 region with conserved amino acids"

XX FT Misc-difference 965

XX FT /note= "Encoded by CGT"

XX PN WO200001819-A1.

XX PD 13-JAN-2000.

XX PF 30-JUN-1999; 99WO-US14944.

XX PR 01-JUL-1998; 98US-0091469.

XX PR 21-JAN-1999; 99US-0116621.

Thu May 8 08:49:37 2003

XX PA (ICAG-) ICAGEN INC.

XX PI Jegla TJ, Wickenden A;

XX DR WPI: 2000-182114/16.

XX DR N-PSDB; AA250119.

XX PT Novel polynucleotides and polypeptides of human ELK, a voltage-gated

XX PT potassium channel subunit useful for treating ELK mis-expression and

XX PT to screen for inhibitors and activators of such channels

XX PS Claim 13; Page 62; 79pp; English.

XX The present sequence is the human ELK (hELK) polypeptide monomer,

XX comprising an alpha subunit of the voltage-gated potassium channel

XX (VGPCs). It is a member of the Kv (Voltage gated potassium) superfamily,

XX Eeg (ether a go-go) family and ELK subfamily of potassium channel

XX monomers. hELK gene is mapped to chromosome 12q13. It is isolated

XX from brain and maintains the resting potential and controls excitability

XX of the cell. It has antimigraine, cerebroprotective, antipsychotic,

XX neuroprotective and anticonvulsant activity. The hELK polypeptide can be

XX used to screen for modulators of VGPCs, that are useful for treating

XX abnormal ion flux disorders, CNS disorders such as migraines, hearing

XX and vision problems, seizures, psychotic disorders and to prevent

XX strokes. It can be used as a marker for diagnosis of diseases linked to

XX this gene and also as reporter molecule in detection systems. The

XX polynucleotide is useful for gene therapy, to rectify ELK expression.

XX SQ Sequence 1083 AA;

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
0	5698.00	1083	1082
Percent Similarity:	99.91%	Conservative:	0
Best local Similarity:	99.91%	Mismatches:	1
Query Match:	93.58%	Indels:	0
DB:	21	Gaps:	0

US-09-965-830-1_COPY_6_3257 (1-3252) x AAY44778 (1-1083)

QY 1 ATGCCGGCCATCGGGGCTCTCTGCGGCTCAGAACACCTTCTGACACCATCGCTAGC 60

DB 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

QY 61 CGTTTCGACGGACGACAGTAACTTCGTCGTCGGGACGCCAGGTGGCGGCTCTTC 120

DB 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40

QY 121 CCCGTGTCTACGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180

DB 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60

QY 181 ATGACGGGGGCTGCTGCT 240

DB 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80

QY 241 CAACAGATCCGCAAGGCCCTGGACGACACCAAGAGTTCAAGGCTGAGCTGATCTGTAC 300

DB 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuLeuTyr 100

QY 301 CGGAAGACGGGCTCCGCT 360

DB 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120

QY 361 GGGAGGTGGCT 420

DB 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140

QY 421 GGGCCCGACAGTGAAGGACAGTGGTGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGG 480

DB 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgArgGlyArgGlyArgGlyArgSer 160

QY 481 AAAGGCTTCAATGCCAACCCGGGCGGAGCGGGCGGCTGCTCTACCACTGTCGGGCGAC 540

DB 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180

QY 541 CTCGAGAAGCAGCCCAAGGCAACGACCACTCAATAAGGGGTGTGGGGAGAAACCA 600

DB 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200

QY 601 AACTTGCTGAGTACAAAGTAGCCGCGCATCCGGAAGTCGCCCTTCATCTCTGTTGCTACTGT 660

DB 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220

QY 661 GGGCACTGAGAGCCACTGGATGGTCTCATCTGCTCGCCACACTCTATGTGGCTGTC 720

DB 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240

QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCAGCAGCGGAGCCAGTGGCGGCGGCGGCGG 780

DB 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260

QY 781 CCCAGCGTCTGTGACCTGGCGGCGTGGAGTCTCTTCATCTCTGACATGTGCTGAATTC 840

DB 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280

QY 841 CGTACCACATTCGTCGTCGCAAGTCGGGCGGCGTGGTGTGGCCCAAGTCCCATTTGCCCTC 900

DB 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300

QY 901 CACTACGTCACACCTGCTCTCTGCTGATGTCATCGAGCGCTGCCCTTTGACCTGCTA 960

DB 301 HistyrValThrThrPheLeuLeuAspValIleAlaLeuProPheAspLeuLeu 320

QY 961 CATGCTCTCAAGTCAAGTGTACTTCGGGCGGCGGCGGCGGCGGCGGCGGCGGCTGCTG 1020

DB 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340

QY 1021 CGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080

DB 341 ArgLeuLeuArgLeuLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360

QY 1081 ACATGCTCATGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140

DB 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380

QY 1141 ATTGGCCAGCGGAGATCGAGACGACGACGACGACGACGACGACGACGACGACGACGACG 1200

DB 381 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400

QY 1201 GAGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1260

DB 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420

QY 1261 AACAGCTCCGCCAGAGTGACAACTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1320

DB 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu 440

QY 1321 GAGTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTC 1380

DB 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460

QY 1381 AGCAGCTCACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1440

DB 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480

QY 1441 TTCTCCATCTGCACATGCTCATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1500

DB 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 500

QY 1501 ACGGCATCATCCAGCGCATGTACGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1560

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Db 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLysGlnArgMetLeuGlu 540
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 Db 541 TyrPheGlnAlaThrTyrAlaValAsnAsnGlyIleAspThrThrGluLeuGlnSer 560
 QY 1681 TCCCTGAGCGAGTCCGCGGACAGATCCGATGCACTGCACAAAGAGGTCTCTGAGGTG 1740
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 QY 1741 CCATGTTTGAAGGGCGGCGGCGGCTGCTGGGGGCACTGTCTGGCCCTGGCGGCC 1800
 Db 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600
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 Db 601 AlaPheCysThrProGlyGlyTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620
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 QY 1981 GAGCTGAAGGGCGTGAAGTACTGCTCAAGGTTGGCGGAGGTGTAAAGGCCAATGCC 2040
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 QY 2401 CCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2460
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 Db 821 SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer 840
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 Db 921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuGlnProLeuCysVal 940
 QY 2821 GACACTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2880
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 QY 3001 GAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3060
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 Db 1021 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 1040
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 Db 1041 ThrGlyGluProProGlySerGlyGlyLeuAlaLeuProTyrAspProHisSerLeu 1060
 QY 3181 GAGATGCTGCTTATGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3240
 Db 1061 GluMetValLeuGlyCysHisGlySerGlyThrValGlnThrThrGlnGluGly 1080
 QY 3241 ACAGGGGCTC 3249
 Db 1081 ThrGlyVal 1083

RESULT 3
 AAY44779
 ID AAY44779 standard; Protein; 1083 AA.
 XX AC AAY44779;
 XX AC AAY44779;
 DT 04-MAY-2000 (first entry)
 XX Human Elk voltage gated potassium channel monomer variant #1.
 DE Voltage gated potassium channel subunit; VGPCs; hElk; human; stroke;
 KW Kv superfamily; Bag family; ether a go-go; Elk subfamily; modulator;
 KW chromosome 12q13; resting potential; cell excitability; seizure; marker;
 KW CNS; migraine; treat; hearing/vision problem; psychotic; anticonvulsant;
 KW ion flux disorder; reporter molecule; detection; gene therapy;
 KW antimigraine; cerebroprotective; neuroprotective; antipsychotic.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 XX Region 452..514
 XX /label= P-S6_region
 XX /note= "Pore-S6 region with conserved amino acids"
 XX Region 452..710
 XX /label= Extended_P-S6_region
 XX /note= "Extended Pore-S6 region with conserved amino acids"
 XX Misc-difference 1065
 XX /note= "Wild type Ile substituted with Val; Ile is stated to be located at 1064 in the specification"


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Region 452..514
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/note= "Pore-S6 region with conserved amino acids"
Region 452..710
/label= Extended_P-S6_region
/note= "Extended Pore-S6 region with conserved amino acids"
Misc-difference 1060
/note= "Wild type Leu substituted with Ile"

WO200001819-A1.
13-JAN-2000.
30-JUN-1999; 99WO-US14944.
01-JUL-1998; 98US-0091469.
21-JAN-1999; 99US-0116621.
(ICAG-) ICAGEN INC.
Jegla TJ, Wickenden A;
WPI; 2000-182114/16.
Novel polynucleotides and polypeptides of human ELK, a voltage-gated potassium channel subunit useful for treating ELK mis-expression and to screen for inhibitors and activators of such channels
Disclosure; Page -: 79pp; English.
The present sequence is the human ELK (hElk) polypeptide variant #2, comprising an alpha subunit of the voltage-gated potassium channel (VGPCs). It is a member of the Kv (Voltage gated potassium) superfamily, Eag (ether a go-go) family and Elk subfamily of potassium channel monomers. hElk gene is mapped to chromosome 12q13. It is isolated from brain and maintains the resting potential and controls excitability of the cell. It has antimigrane, cerebroprotective, antipsychotic, neuroprotective and anticonvulsant activity. The hElk polypeptide can be used to screen for modulators of VGPCs, that are useful for treating abnormal ion flux disorders, CNS disorders such as migraines, hearing and vision problems, seizures, psychotic disorders and to prevent strokes. It can be used as a marker for diagnosis of diseases linked to this gene and also as reporter molecule in detection systems. The polynucleotide is useful for gene therapy, to rectify ELK expression.
Note: The present sequence is not found in the specification but derived from hELK amino acid sequence found in page 62.
XX
XX
SQ Sequence 1083 AA;

Alignment Scores:
Pred. No.: 0 Length: 1083
Score: 5696.00 Matches: 1081
Percent Similarity: 99.91% Conservative: 1
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 93.55% Indels: 0
DB: 21 Gaps: 0

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QY 61 CGCTTCACGGCAGCACAGTAACCTTCGTGGCCACGCCAGGTGGCGGGCTCTTC 120
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40
QY 121 CCCTGTGCTTACTGCTCTCTGATGGCTTCTGTGACCTCAGCGGGTCTCCCGGGCTGAGTC 180
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QY 181 ATCAGCGGGGCTGTGGCTCTCTCTCTTATGGGCCACAGCACCACTGAGCTCGTCGCG 240

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81	GlnGlnIleArgGlyAlaLeuAspGluHisGlyGluPheLysAlaGluLeuIleLeuTyr	100
301	CGGAAGACGGGCTCCCGTTCTGTGTCTCTCTGATGTATACCATCAAAAGAAATAGAAA	360
101	ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys	120
361	GGGAGGTGGCTCTCTCTCTAGTCTCTCACAGGACATCAGCAAAACCAAGACCGAGGG	420
121	GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly	140
421	GGCCCGACAGATGAAAGGAGACAGTGGTGGCGGCGCCGATGATGCGGGCGGCAGTCC	480
141	GlyProAspArgTrpLysGluThrGlyGlyArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis	160
481	AAAGGCTTCAATGCCAACCGCGGGGAGCGGGCGGTGCTTACCACCTGTCGGGCAC	540
161	LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis	180
541	CTGCAGAAGCAGCCCAAGGGCAAGCAAGTCATAGGGGGTGTGGGGAGAAACCA	600
181	LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro	200
601	AACTGGCTGAGTACAAAGTAGCCGCCATCCGAGTCGCCCTCATCTGTGTGACACTGT	660
201	AsnLeuProGluTyrLysValAlaIleArgLysSerProPheIleLeuLeuHisCys	220
661	GGGCACGTGAGACCCACCTGGATGCTCATCTCTGCCACACTCATGTGGCTGTC	720
221	GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal	240
721	ACTGTGCCCTACAGCGTGTGTGAGCACAGCAGGAGCCAGTCGCCGCCGGCGCCG	780
241	ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro	260
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261	ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe	280
841	CGTACCAATCTGTCTCAAGTCGGCGGTGGTGTTCGCCCAAAGTCATTTGCCCTC	900
281	ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu	300
901	CACCTAGTCAACCACTGGTCTCTGATGTATCATCGACGCTGCCCTTTGACCTGCTA	960
301	HisTyrValThrThrTrpPheLeuLeuAspValIleAlaLeuProPheAspLeuLeu	320
961	CATGCTTCAMAGTCAAGTCAGTCTCTCGGGCCCATCTGTGAAGCGGTGCGCTGCTG	1020
321	HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu	340
1021	CGCTGCTCGGCTGCTTCCGCGGTGACCGGTACTCGCAGTACAGCGCGGTGGCTG	1080
341	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu	360
1081	ACACTGCTCATGGCGGTGTTCCCTGTCGGGCACTGGGTGGCTGGCTGGTTTAC	1140
361	ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr	380
1141	ATTGGCCAGCGGAGATCGAGACGACGGAATCCGAGCTCCCTGAGATGGCTGGCTGAG	1200
381	IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln	400
1201	GAGTGGCCCGCACTGGAGACTCCCTACTACTGTGGCGGCGGAGCCAGCTGGAGGG	1260
401	GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly	420
1261	AACAGTCCGGCCAGAGTGAACAACCTCAGCAGCAGCAGCGAGGCCAACCGGCGGTG	1320

Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu 440
 QY 1321 GAGTGTGGGGGGCCCTGCTGGCAGCGCTACATACATCCCTCTCTACTTCCCATC 1380
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 QY 1381 AGCAGCTCACACCGTGGGCTTGGCAACGTGTCGCAACAGCGGACACGAGAGATC 1440
 Db 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGlnLysIle 480
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 Db 501 ThrAlaIleIleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgAsp 520
 QY 1561 CTGGCGGACTATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 1620
 Db 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLysGlnArgMetLeuGlu 540
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 QY 1741 CCACTCTTTGAGCGGCCAGCGCGCTGCTCGCGGCGACTGCTGCGCGCTGCGCGCC 1800
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RESULT 5
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 ID AAY84835 standard; Protein; 1083 AA.
 XX AC AAY84835;
 XX AC
 DT 08-AUG-2000 (first entry)
 XX
 DE Herg4, a potassium channel protein of the ERG family.
 XX Human; potassium channel protein; Herg4; human erg related gene 4;
 KW epilepsy; migraine; cell proliferation disorder; cancer;

KW compermental trouble; neurotransmitter; hormone; ischemia;
 KW brain disease; cardiac disease; inflammation; pain.
 XX Homo sapiens.
 OS WO200022001-A2.
 XX 20-APR-2000.
 XX 13-OCT-1999; 99WO-EP07671.
 XX 13-OCT-1998; 98EP-0402540.
 PR (SNFI) SANOFI-SYNTHELABO.
 PA Renard S, Avenet P;
 XX WPI; 2000-317948/27.
 DR N-PSDB; AAA14893.
 XX Novel herg4 polypeptide of human erg potassium channel family useful
 PT for treatment of epilepsy, migraine, cell proliferation
 XX Claim 11; Page 45-48; 48pp; English.
 XX The present sequence represents a human potassium channel protein of
 CC the ERG family, which is designated Herq4 (human erg related gene 4).
 CC The Herq4 polypeptides and polynucleotides are useful in the treatment
 CC of epilepsy, migraine, cell proliferation disorders, cancer,
 CC compermental troubles, and to prevent or alter the effect of
 CC endogenous neurotransmitters and hormones. Antibodies against
 CC Herq4 are also useful for the treatment of cerebral, cardiac and renal
 CC ischemias, brain and cardiac diseases, inflammation, pain, and to mimic
 CC or antagonize the effect of endogenous neurotransmitters and hormones.
 XX SQ Sequence 1083 AA;

Alignment Scores:
 Pred. No.: 0 Length: 1083
 Score: 5695.00 Matches: 1081
 Percent Similarity: 99.91% Conservative: 1
 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 93.53% Indels: 0
 DB: 21 Gaps: 0

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QY 1 ATGCGCGCCATCGGGGCTCTCTGGCGCTCAGACACCTTCTGACACCATCGCTAGG 60
 DB 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
 QY 61 CGCTTCGACGGCAGCAGCAGTAACTCGTGGGCAACGCCAGCGCGGGGCTCTTC 120
 DB 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40
 QY 121 CCCTGCTCTACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
 QY 181 ATGACAGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80
 QY 241 CAACAGATCGCAAGCCCTGGAGCAGCAGAGTTCAGGCTCAAGCTGAGCTGATCCTGTAC 300
 DB 81 GlnGlnIleArgGlyAlaLeuAspGluHisGlyLeuPheValGluLeuIleLeuTyr 100
 QY 301 CGAAGAGCGGGCTCCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 101 ArgGlySerGlyLeuProPheTyrPcysLeuLeuAspValIleProIleLysAsnGluLys 120
 QY 361 GGGAGGTGGCT 420

DB 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140
 QY 421 GGCCCGCAGATGGAAGAGAGACAGTGTGGCGCGCGGATATGCGCGGACCATCC 480
 DB 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgTrpGlyArgAlaArgSer 160
 QY 481 AAAGGCTTCAATGCCAACCGCGGCGGAGCGCGGCTCTACACCATGTCGGGCAC 540
 DB 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
 QY 541 CTGCAAGCAGCCCAAGGCAAGCAACGCTCAATAAGGGGTGTTGGGAGAAACCA 600
 DB 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200
 QY 601 AACTGCTCTAGTACAAAGTAGCGCATCGGAAGTCGCCCTTCATCTCTGCTGCTGCT 660
 DB 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220
 QY 661 GGGCACTGAGACACCTGGGATGCTTCATCTGCTGCGCCACACTCTATGTGGCTGC 720
 DB 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
 QY 721 ACTGTGCCCTACAGCGT 780
 DB 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
 QY 781 CCCAGCTCTGTGACCTGGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
 DB 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280
 QY 841 CGTACCACATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 900
 DB 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300
 QY 901 CACTAGTCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 DB 301 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaLeuProPheAspLeuLeu 320
 QY 961 CATGCTTCAAGGTCAAGTGTACTTCGGGGCCCATCTGCTGCAACGCGTGGCGCTGCTG 1020
 DB 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340
 QY 1021 CGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 DB 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360
 QY 1081 ACAGTCTCATGGCGTGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 DB 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380
 QY 1141 ATGGCCAGCGGAGATCGAGAGCAGCAGCAATCGAGCTGCCTGAGATTGGCTGGCTGAG 1200
 DB 381 IleGlyGlnArgGluLeuGluSerGluSerGluLeuProGluIleGlyTrpLeuGln 400
 QY 1201 GAGCTGGCGCGCTGAGAGTCCCTACTACTACTGCTGGCGCGGAGCGCCAGCTGAGGG 1260
 DB 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420
 QY 1261 AACAGCTCGCGCAGAGTGCACAACTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1320
 DB 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu 440
 QY 1321 GAGCTGTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 DB 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460
 QY 1381 AGCAGCTCACAGCTGGGCTGCGCAACGTGTCCGCCAACACGCGACACCGAGAGATC 1440
 DB 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480
 QY 1441 TTCTCCATCTGCACATGCTCATCGCGCGCTGATGACGCGGTGTGTGTGTGTGTGTGTGTGT 1500
 DB 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValPheGlyAsnVal 500

QY	1501	ACGCCATCATCCAGCCGATGTACGCCCGCGCTTCTGTACACAGCCCGCAGCGGGAC	1560
Db	501	ThrAlaIleIleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgasp	520
QY	1561	CTGCGCGACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1620
Db	521	LeuArgAspTyrIleArgIleHisArgIleProIysProLeuIysGlnArgMetLeuGlu	540
QY	1621	TACTTCAGCGCCACCTGGGGCGGTGACATGGCATCGACACCAACCCAGCTGTCAGAGC	1680
Db	541	TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuGlnSer	560
QY	1681	CTCCCTGACGAGCTGGCGCGCAGACATCGCATCCACTGCACAGGAGTCTCGACGTG	1740
Db	561	LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisIysGluValLeuGlnLeu	580
QY	1741	CCACTGTTTGAGCGCGCCAGCGCGCTGCTCGCGGGCACTGCTCTGCGCCCTGGGGCCC	1800
Db	581	ProLeupheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro	600
QY	1801	GCCTTCTGCAGCGCGCGGCGAGTACCTATCCACCAAGCGATGCCCTGCAGGCCCTCTAC	1860
Db	601	AlaPheCysThrProGlyIuTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr	620
QY	1861	TTTGCTGCTGCTGCTCCATGAGGTGCTCAAGGTGGCCGCTGCTCGCCATCTCAGGG	1920
Db	621	PheValCysSerGlyPheMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly	640
QY	1921	AAGGGGACCTGATCGCTGCTGAGCTGCCCGGGGAGCAGGTGGTAAAGGCCAATGCC	1980
Db	641	LysGlyAspLeuIle66IYCysGlnLeuProArgGluGlnValValLysAlaAsnAla	660
QY	1981	GAGGTGAAGGGGCTCAGCTACTGCTGCTGCAGTGTCTGCAGCTGCTGCAGTGGCTGCACGAC	2040
Db	661	AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp	680
QY	2041	AGCCTTGGCTGTACCCGAGTTTGCCCGCGCTTCAGTCTGCGCTCCGAGGGGAGCTC	2100
Db	681	SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu	700
QY	2101	AGCTACACCTGGGTGCTGGGGAGGTCTGCAGAGTGGACACAGCTCCCTCAGCGGC	2160
Db	701	SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly	720
QY	2161	GACAAATACCTTATGTCACGCTGGAGGAGACAGACAGATGGGGAGCAGGGCCCCACG	2220
Db	721	AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr	740
QY	2221	GTCTCCCGAGCCCGAGTGTATGAGCCCTCCAGGCCCTGCTGTGCTCCCTGCTGCTCC	2280
Db	741	ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer	760
QY	2281	TCATCTCTAGTGCACAGCTGCTATCCCGCATCGTGAACAGACCCCGCTCGCTAGGT	2340
Db	761	SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly	780
QY	2341	GGCAGAGGGAGCCAGCGAGGCGGGGCTTTGAGGCTGAGGCTGGCCCTCTGCTGCC	2400
Db	781	GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro	800
QY	2401	CCAGGGCCCTAGAGGGGCTACGGCTGCCCGCCCATCGCATGGAAATGTGCCCCAGATCTG	2460
Db	801	ProArgAlaLeuGluGlyLeuArgLeuProProMetProTyrAsnValProProAspLeu	820
QY	2461	AGCCCCAGGCTAGATGATGGCATTAAGAGCGGTGGCTCGCGACCGCCCGAAGTCTCT	2520
Db	821	SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer	840
QY	2521	TTCCGCGTGGCGCAGTCTGCGCCGGAATGTAGCAGCAGGCCCTCCCGCTCGACACGAGCC	2580
Db	841	PheArgValGlyGlnSerGlyProGluCysSerSerProSerProGlyProGluSer	860

Qy	2581	GGCTGTCTCACTGTTCCTCATGTGGCCCGCCAGGACGAGGACACAGACACACTGGACAAG	2640
Db	861	GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys	880
Qy	2641	CTTCGGAGCGCGTTCACAGACTCTCAGACGAGTGTCTGCAGATGCGGGAGGAGTCTCAG	2700
Db	881	LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln	900
Qy	2701	TCACTTCGCACAGGCTGTGCAGCTTGTCTCTGGCGCCACAGAGGAGGCTCCGTGCCCTCGG	2760
Db	901	SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg	920
Qy	2761	GCATCGGAGAGGGCGCTGCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTG	2820
Db	921	AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysLeu	940
Qy	2821	GACACTGGGCATCTCTCTACTCTGCCTGCAGCCCGCCAGCTGGCTGTCTTGTGAGTGGGACT	2880
Db	941	AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr	960
Qy	2881	TGGCCCCACCTCTCTCGGGGCTCTCTCCCTCATGGCACCTTGGACCTCCACCTCAGACTCA	2940
Db	961	TrpProHisProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProPro	980
Qy	2941	CGCTCTCAGAGTCCCTCGGCTCGAGCCACACAGCTTCTTGGACCTCCACCTCAGACTCA	3000
Db	981	AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer	1000
Qy	3001	GAGCCCCCTGCCTCAGAGACCTCTCTCTGAGCCAGCACCCCTGCCCTCCCTCTCTCT	3060
Db	1001	GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro	1020
Qy	3061	TCTGAGAAAGGGCTAGGACTGGGCGCCGAGAGCTGTGAGCCAGCTGTGAGCCAGCTACCCAGC	3120
Db	1021	SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer	1040
Qy	3121	ACTGGAGAGCCCCACAGGGTTCAGGGGCTGGCTTGGCTGGGACCCACAGCCCTG	3180
Db	1041	ThrGlyGluProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu	1060
Qy	3181	GAGATGGTCTTATTGGCTGCATGGCTCTGGCACAGTCCAGTGGACCCAGGAGGAAGGC	3240
Db	1061	GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly	1080
Qy	3241	ACAGGGGTC 3249	
Db	1081	ThrGlyVal 1083	
RESULT	6		
AA	AA44781		
ID	AA44781	standard; Protein; 1083 AA.	
XX	AC	AA44781;	
XX	DT	04-MAY-2000 (first entry)	
XX	DE	Human Elk voltage gated potassium channel monomer variant #3.	
KW	KW	Voltage gated potassium channel subunit; VGPCs; helx; human; stroke;	
KW	KW	Kv superfamily; Eag family; ether a go-go; Elk subfamily; modulator;	
KW	KW	chromosome 12q13; resting potential; cell excitability; seizure; marker	
KW	KW	CNS; migraine; treat; hearing/vision problem; psychotic; anticonvulsant	
KW	KW	ion flux disorder; reporter molecule; detection; gene therapy;	
XX	XX	antimigrane; cerebroprotective; neuroprotective; antipsychotic.	
OS	OS	Homo sapiens.	
XX	XX	Synthetic.	
Key	Key	Location/Qualifiers	
FT	FT	452..514	
FT	FT	/label= p-S6_region	
FT	FT	/note= "Pore-S6 region with conserved amino acids"	
FT	FT	452..710	

FT /label- Extended_P-S6_region
 FT /note- "Extended Pore-S6 region with conserved amino
 FT acids"
 FT Misc-difference 744
 FT /note- "Wild type Ala substituted with Ser"
 XX
 PN WO200001819-A1.
 XX
 PN 13-JAN-2000.
 XX
 XX 30-JUN-1999; 99WO-US14944.
 XX
 XX 01-JUL-1998; 98US-0091469.
 XX
 XX 21-JAN-1999; 99US-0116621.
 XX
 XX (ICAG-) ICAGEN INC.
 XX
 XX Jegla TJ, Wickenden A;
 XX
 XX WPI; 2000-182114/16.
 XX
 XX Novel polynucleotides and polypeptides of human ELK, a voltage-gated
 XX potassium channel subunit useful for treating ELK mis-expression and
 XX to screen for inhibitors and activators of such channels
 XX
 XX Disclosure; Page -: 79pp; English.
 XX
 XX The present sequence is the human ELK (hELK) polypeptide variant #3,
 XX comprising an alpha subunit of the voltage-gated potassium channel
 XX (VGPCs). It is a member of the Kv (Voltage gated potassium) superfamily,
 XX Eag (either a go-go) family and Elk subfamily of potassium channel
 XX monomers. hELK gene is mapped to chromosome 12q13. It is isolated
 XX from brain and maintains the resting potential and controls excitability
 XX of the cell. It has antimigraine, cerebroprotective, antipsychotic,
 XX neuroprotective and anticonvulsant activity. The hELK polypeptide can be
 XX used to screen for modulators of VGPCs, that are useful for treating
 XX abnormal ion flux disorders, CNS disorders such as migraines, hearing
 XX and vision problems, seizures, psychotic disorders and to prevent
 XX strokes. It can be used as a marker for diagnosis of diseases linked to
 XX this gene and also as reporter molecule in detection systems. The
 XX polynucleotide is useful for gene therapy, to rectify ELK expression.
 XX Note: The present sequence is not found in the specification but
 XX derived from hELK amino acid sequence found in page 62.
 XX
 XX Sequence 1083 AA;
 SQ
 Alignment Scores:
 Pred. No.: 0 Length: 1083
 Score: 5695.00 Matches: 1081
 Percent Similarity: 99.91% Conservative: 1
 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 93.53% Indels: 0
 DB: 21 Gaps: 0
 US-09-965-830-1_COPY_6_3257 (1-3252) x AAY44781 (1-1083)
 QY 1 ATCCCGGCATCGGGGCTCTCTGGGCTCTGAGACACCTCTCTGACACCATCGCTACG 60
 Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
 QY 61 CGCTTCGACGGCACACGACATCTCTGCTGGGACGCCCGGAGTGGCGGGCTCTTC 120
 Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40
 QY 121 CCGTGGTCTACTGCTGATGCTCTCTGACCTCAGCGGCTCTCCCGGCTGAGGTC 180
 Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
 QY 181 ATCAGCGGGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
 Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80
 QY 241 CAACAGATCCGACGAGCCCTGGACGACACAAAGAGTTCAAGGCTGAGCTGATCCTGTAC 300

Db 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuLeuLeuTyr 100
 QY 301 CGGAAGAGCGGGCTCCGCTCTGCTGCTCTGATGATGATGATGATGATGATGATGATG 360
 Db 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120
 QY 361 GGGAGGTGCT 420
 Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140
 QY 421 GGGCCCGACAGATGGAAGGACAGAGGTGGTGGCGGCGCGGATGATGATGATGATGATG 480
 Db 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgArgArgArgArgArgArgArg 160
 QY 481 AAGGCTTCAATGCCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
 Db 161 LysGlyPheAsnAlaAsnArgArgArgArgArgArgArgArgArgArgArgArgArg 180
 QY 541 CTGACAGACGACCCCAAGGCAAGCAAGCTCAATAGGGGTGTGGGAGGAGCAACCA 600
 Db 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200
 QY 601 AACTGCTGAGTAAAGTAGCCGATCGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 660
 Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220
 QY 661 GGGGCACTGAGACGACCTGGGATGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
 Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
 QY 721 ACTGTGCCCTACAGCGTGTGTGAGCAGACAGCGGAGCGGAGCGGAGCGGAGCGGAG 780
 Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
 QY 781 CCCAGCGTGTGACCTGGCGCTGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
 Db 261 ProSerValCysAspLeuAlaValGluValPheIleLeuAspIleValLeuAsnPhe 280
 QY 841 CGTACCACTTCGTCGCAAGTCCGCGGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 900
 Db 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300
 QY 901 CACTAGTCACACCTGCT 960
 Db 301 HistyrValThrThrPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320
 QY 961 CATGCTTCAAGGTCAACGTGTACTTGGGGGCGCATCTCTCTCTCTCTCTCTCTCTCTCT 1020
 Db 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340
 QY 1021 CGCTCTCGCTGCT 1080
 Db 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360
 QY 1081 ACACCTCTCATGGCGCTGTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCTCT 1140
 Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380
 QY 1141 ATGGGCGAGCGGAGATCGAGAGCAGCAGCAATCCGAGCTGCTGAGATTGGCTGGTCGAG 1200
 Db 381 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400
 QY 1201 GAGCTGGCGCGCGCTGAGACTCCCTACTACTCTGCTGGCGGCGGAGCGGAGCGGAG 1260
 Db 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420
 QY 1261 AACAGCTCCGCGCAGAGTGACACTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1320
 Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 440
 QY 1321 GAGCTGCTGGCGCGCGCTGCTGCGCAGCGCTCTACATCACCTCCCTCTCTCTCTCTCT 1380

Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460
QY 1381 AGCAGCCTCACCAGCGTGGCTTCGCGCAACGCTGTCGCCCAACACGACCGGAGAGATC 1440
Db 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480
QY 1441 TTCTCCATGTCACCATGCTCATCGCGCCCTGATCGACGCGGTGTGTTTGGACGCTG 1500
Db 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValPheGlyAsnVal 500
QY 1501 ACGCGCATCATCCAGCGATGACGCGCGCGCTTCTGTACACAGCGCGCGCGAC 1560
Db 501 ThrAlaIleIleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgasp 520
QY 1561 CTGCGCGACTACATCCGATCCACCGTATCCCAAGCCCTCAACAGCGCATGCTGGAG 1620
Db 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540
QY 1621 TACTTCCAGGCGACCTGGCGGTGAACAATGCAATGCAATGCAATGCAATGCAATGCAAT 1680
Db 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuGlnSer 560
QY 1681 CTCCCTGACGAGCTGCGCGACAGATCCCATGCCATGCCATGCCATGCCATGCCATGCC 1740
Db 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGlnValLeuGlnLeu 580
QY 1741 CCACCTGTTGAGCGCGCGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGC 1800
Db 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600
QY 1801 GCCTTCTGCGCGCGCGCGAGTACTCATCCACCAAGCGGATGCCCTGCGGCGCTGCTAC 1860
Db 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620
QY 1861 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Db 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640
QY 1921 AAGGGCACTGATCGGCTGTAGCTGCCCGCGCGGAGGAGTGGTAAGGCGCAATGCC 1980
Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 660
QY 1981 GACGTGAAGGGGTGACGTACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
Db 661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680
QY 2041 AGCTTTGCGCTGACCCGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
Db 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700
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Db 701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720
QY 2161 GACATACCTTATGCTCCACGCTGAGGAGAGAGACAGATGGGAGAGGCGCCACG 2220
Db 721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740
QY 2221 GTCTCCGAGCGCGCTGATGAGCGCTCCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
Db 741 ValSerProSerProAlaAspLupProSerProLeuLeuSerProGlyCysThrSer 760
QY 2281 TCATCTCAGTCCGACGCTATCCCGATCCCGATCCCGATCCCGATCCCGATCCCGATCC 2340
Db 761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780
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QY 2401 CCAGGCGCGCTAGAGGCGCTGAGGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGC 2460
Db 801 ProArgAlaLeuGluGlyLeuArgLeuProProMetProTyrAsnValProProAspLeu 820

QY 2461 AGCCCGAGGGTACTAGATGCGCATTTAGAGCGGTGTGGCTCGGACCGCCCAAGTTCTCT 2520
Db 821 SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer 840
QY 2521 TTCCGCGTGGCGAGTCTGGCGCGGAATGTAGCAGCAGCCCTCCCTGCGACAGAGAGC 2580
Db 841 PheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer 860
QY 2581 GGCCTGCTCAGTGTTCCTCCATGGCCCGCGAGCGAGGAGGAGGAGGAGGAGGAGGAG 2640
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QY 2641 CTTCCGAGCGCGTGCACAGCTGTGCAGAGCGTGTGCAGATGCGGAGGAGGAGGAGGAG 2700
Db 881 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 900
QY 2701 TCACCTTGGCGAGCGTGTGCAGCTTGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 2760
Db 901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 920
QY 2761 GCATCGGAGAGGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2820
Db 921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 940
QY 2821 GACACTGGGCGATCCTCTACTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2880
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QY 2881 TGGCG 2940
Db 961 TrpProHisProAlaProGlyProProProLeuMetAlaProTrpProTrpGlyProPro 980
QY 2941 GCGTCTCAGAGCTCCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3000
Db 981 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000
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Db 1021 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 3180
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Db 1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060
QY 3181 GAGATGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGluGly 1080
QY 3241 ACAGGGGCTC 3249
Db 1081 ThrGlyVal 1083

RESULT 7

AAAY77738

ID AAAY77738 standard; Protein; 1080 AA.

XX AAAY77738;

AC AAAY77738;

XX 19-MAY-2000 (first entry)

XX Human ESK1 (HESK1) protein.

DE Human ESK1 (HESK1) protein.

XX ESK1; eag similar K⁺ channel; potassium channel associated disorder;

KW neurological; Alzheimer's disease; anxiety; panic; autism; hyperactivity;

KW obsessive-compulsive disorder; schizophrenia; Huntington's disease;

KW epilepsy; cardiovascular; musculoskeletal; proliferative; cancer;

KW ESK channel blocker; nootropic; neuroprotective; antidepressant;

KW tranquilizer; neuroleptic; antiParkinsonian; cardiant; cyrostatic;

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.41% Indels: 0
 DB: 21 Gaps: 0

US-09-965-830-1_COPY_6_3257 (1-3252) x AAY77738 (1-1080)

QY 10 ATCGGGGCTCTGGCGCTCAGACACACCTTCTTGACACCATCGCTAGCGCTTCGAC 69
 Db 1 MetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThrArgPheAsp 20
 QY 70 GGCACGACAGTAACCTTCGTCTGGCAACGCCAGAGTGGGGGGCTCTCCCGCTGCTC 129
 Db 21 GlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPheProValVal 40
 QY 130 TACTGCTCTGATGGCTTCTGTGACCTCAGGGCTTCTCCGGGCTGAGGTACATCAGCGG 189
 Db 41 TyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluValMetGlnArg 60
 QY 190 GGCTGTGCTCTCTCTCTTATGGCCAGACACACAGTGTGCTGCTCGCCAAACAGATC 249
 Db 61 GlyCysAlaCysSerPheLeuThrGlyProAspThrSerGluLeuValArgGlnGlnIle 80
 QY 250 CGCAAGGCCCTGGAGCAGCACAAGAGTTCAGAGCTGAGCTGATCTCTACCGGAAGAGC 309
 Db 81 ArgGlyAlaLeuAspGluHisGlyGluPheLysAlaGluLeuLeuTyrArgLysSer 100
 QY 310 GGGTCTCCGCTTCTGCTGCTCTCTGATGTATACCATTAAGATGAGAAAGGGAGGTG 369
 Db 101 GlyLeuProPheThrCysLeuLeuAspValIleProLleLysAsnGluLysGlyGluVal 120
 QY 370 GCTCTCTTCCTAGTCTCTCAAGGACATCAGCAGAAACCAAGACCGGGGGCCCCGAC 429
 Db 121 AlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGlyGlyProasp 140
 QY 430 AGATGAAGGACAGAGTGGTGGCGGGCGCGATATGGCGGGCAGATCCAAAGGCTTC 489
 Db 141 ArgTrpLysGluThrGlyGlyArgArgTrpGlyArgAlaArgSerLysGlyPhe 160
 QY 490 AATGCCAACCGGGCGGAGCGCGCTCTACCATCTGTCGGGGCAGCTGCAAGAG 549
 Db 161 AsnAlaAsnArgArgArgSerArgAlaValLeuTyrHisLeuSerGlyHisLeuGlnLys 180
 QY 550 CAGCCCAAGGCAAGCACAAGCTCAATAAGGGGGTGTGGGAGAGAAACCAATGCTCCT 609
 Db 181 GlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGlyLysProAsnLeuPro 200
 QY 610 GAGTACAAAGTACGCCCATCCGGAAGTGGCGCTTCTATCTGTGCTGCTGCTGCTGCTG 669
 Db 201 GluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCysGlyAlaLeu 220
 QY 670 AGAGCCACCTGGGATGGCTCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 729
 Db 221 ArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaValThrValPro 240
 QY 730 TACAGCTGTGTGTGACAGCAGCAGGAGCGCCAGTGCCTCCCGCGCGCGCGCGCGCGCTC 789
 Db 241 TyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyProSerVal 260
 QY 790 TGTGACCTGGCGGTGGAGGTCTCTTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 849
 Db 261 CysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPheArgThrThr 280
 QY 850 TTCGTGTCTTCCAGTGGCGGCGAGGTGCTGTTTCCCGCCCAAGTCCATTTCCTCCACTAGCTC 909
 Db 281 PheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeuHisIleVal 300
 QY 910 ACCACCTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969
 Db 301 ThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeuHisAlaPhe 320
 QY 970 AAGGTCAACGTGTACTTCGGGGCGCATCTGCTGAAGAGCGGTGCGGCTCTCTGCGGCTGCTG 1029

anticonvulsant.
 Homo sapiens.
 Key Location/Qualifiers
 Domain 212..239
 /note= "potential transmembrane domain S1"
 Domain 259..277
 /note= "potential transmembrane domain S2"
 Domain 297..320
 /note= "potential transmembrane domain S3"
 Domain 329..349
 /note= "potential transmembrane domain S4"
 Domain 356..378
 /note= "potential transmembrane domain S5"
 Modified-site 418
 /note= "potential N-glycosylation site"
 Modified-site 425
 /note= "potential N-glycosylation site"
 Modified-site 433
 /note= "potential N-glycosylation site"
 Domain 449..468
 /note= "potential pore-forming P domain"
 Modified-site 467
 /note= "potential N-glycosylation site"
 Domain 477..501
 /note= "potential transmembrane domain S6"
 Modified-site 496
 /note= "potential N-glycosylation site"
 Domain 601..668
 /note= "putative cyclic nucleotide binding domain (CNBD)"
 WO200009534-A1.
 24-FEB-2000.
 13-AUG-1999; 99WO-US18556.
 14-AUG-1998; 98US-0096570.
 (ELAN-) ELAN PHARM INC.
 Forsayeth JR, Zhao BB;
 WPI; 2000-224270/19.
 N-PSDB; AAZ87712.
 Novel eag similar potassium channel polypeptide useful for treating various neurological, cardiovascular, musculoskeletal and proliferative disorders
 Claim 3; Fig 1A-E; 52pp; English.
 This represents a eag similar K+ channel (ESK) polypeptide (hESK1). The hESK1 protein can be expressed by standard recombinant methodology. The ESK polypeptide, polynucleotides and antibodies are useful for treating and diagnosing various potassium channel associated disorders such as neurological disorders, e.g. Alzheimer's disease, depression, anxiety, panic, obsessive-compulsive disorders, attention deficit, epilepsy; Parkinson's disease, autism, schizophrenia, Huntington's disease and hyperactivity disorders, cardiovascular disorders, musculoskeletal disorders and proliferative disorders such as cancer. The ESK polynucleotide is also useful for synthesis of ESK and gene mapping. The polypeptide can be used in an assay to identify molecules such as synthetic drugs, the antibodies, peptides or other molecules which have an effect on the activity of the ESK channel.

Sequence 1080 AA;
 Alignment Scores: 0 Length: 1080
 Pred. No.: 5688.00 Matches: 1080
 Score:

Db 321 LysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeuArgLeuLeu 340
 QY 1030 GCCCTGCTTCCGCGCTGACCGGTACTCGCAGTACAGCGCGGTGCTGCTGACACTGCTC 1089
 Db 341 ArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeuThrLeuLeu 360
 QY 1090 ATGGCCGTGTCGCGCTGCTCGCGCACTGGGTGGCTCGCTCGCTGCTGCTTACATGGCCAG 1149
 Db 361 MetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyrIleGlyGln 380
 QY 1150 CGGAGATCGAGAGCAGCAATCCGAGCTGCTGAGATGGCTGCTGCTGCTGCTGCTGCTGCTG 1209
 Db 381 ArgGlnIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGlnLeuAla 400
 QY 1210 CGCGACTGGAGACTCCCTACTACTGCTGGCGGAGCGCCAGCTGGAGGAAAGACTGCC 1269
 Db 401 ArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGlyAsnSerSer 420
 QY 1270 GGCAGAGTGACAACTGCAGCAGCAGCAGCGCCACAGCGGAGCGGCTGCTGCTGCTGCTG 1329
 Db 421 GlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeuGluLeuLeu 440
 QY 1330 GCGCGCCGCTGCTGCGCGAGCGCTACATCACTCCCTACTTCCGACTCGAGCGCTC 1389
 Db 441 GlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeuSerSerLeu 460
 QY 1390 ACCAGCTGGGCTTCGCGACGCTGTCGCGCAACAGCAGCAGCGAGAGATCTTCTCCATC 1449
 Db 461 ThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIlePheSerIle 480
 QY 1450 TGCACTGCTCATCGCGCGCTGATGACCGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1509
 Db 481 CysThrMetLeuIleGlyAlaLeuMetHisAlaValPheGlyAsnValThrAlaIle 500
 QY 1510 ATCCAGCGATGACCGCGCGCTTCTGTACACAGCGCGCGCGCGCGCGCGCGCGCGCG 1569
 Db 501 IleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAspLeuArgAsp 520
 QY 1570 TACATCCGATCCACCGTATCCCAAGCCCTCAACAGCGAGTGTGCTGCTGCTGCTGCTGCTG 1629
 Db 521 TyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGluTyrPheGln 540
 QY 1630 GCACCTGGCGGTGACATGCCATGCGATCGACACCGAGTGTGCTGCTGCTGCTGCTGCTGCTG 1689
 Db 541 AlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSerLeuProAsp 560
 QY 1690 GAGCTGGCGGACATGCCATGCGATCGACACCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1749
 Db 561 GluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeuProLeuPhe 580
 QY 1750 GAGCGCGCAGCGCGGTGCTGCTGCGGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1809
 Db 581 GluAlaLeuSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgProAlaPheCys 600
 QY 1810 AGCGCGCGAGTACCTCATCCACCAAGCGATGCGCTGCGAGCGCTGCTGCTGCTGCTGCTGCT 1869
 Db 601 ThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyrPheValCys 620
 QY 1870 TCTGCTCATGGAGTGTCAAGGTGGCAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1929
 Db 621 SerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGlyLysGlyAsp 640
 QY 1930 CTGATCGCTGTGAGTCCCGCGGAGCAGGTGTGTAAGGCCAATGCCAGCTGAAG 1989
 Db 641 LeuIleGlyCysGluLeuProArgGluGlnValValLysAlaAsnAlaAspValLys 660
 QY 1990 GGGCTGAGTACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2049
 Db 661 GlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAspSerLeuAla 680
 QY 2050 CTGTACCCCGAGTTGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2109
 Db 681 LeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeuSerTyrAsn 700

QY 2110 CTGGGTGCTGGGGAGGCTCTGTCAGAGGTGGACACAGCTCCTGAGCGGCGACAATACC 2169
 Db 701 LeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGlyAspAsnThr 720
 QY 2170 CTTATGTCCACGCTGAGGAG 2229
 Db 721 LeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThrValSerPro 740
 QY 2230 GCGCCAGCTGATGAGCCCTCCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2289
 Db 741 AlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSerSerSerSer 760
 QY 2290 GCTGCAAGCTGCTATCCCACTCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2349
 Db 761 AlaAlaLysLeuLeuSerProArgThrAlaProArgProArgLeuGlyGlyArgGly 780
 QY 2350 AGCCAGCAGCGGCGGCTTTGAAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 2409
 Db 781 ArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaProProArgAla 800
 QY 2410 CTAGAGGGCTACGGCTGCCCCCATGTCATGGAATGTGCCACAGATCTGAGCCCGCAGG 2469
 Db 801 LeuGluGlyLeuArgLeuProProMetProTrpAsnValProAspLeuSerProArg 820
 QY 2470 GTAGTACATGCATTGAAGCGGTGTGCTGCGACAGCCCAAGTCTCTTTCGCGCTG 2529
 Db 821 ValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSerPheArgVal 840
 QY 2530 GGCAGTCTGGCGGATGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2589
 Db 841 GlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSerGlyLeuLeu 860
 QY 2590 ACTGTTCCCATGGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2649
 Db 861 ThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLysLeuArgGln 880
 QY 2650 GCGGTGACAGAGTGTGACAGCAGTGTGCTGATGGGGAAGGACACACACTGGACACTTTCG 2709
 Db 881 AlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGlnSerLeuArg 900
 QY 2710 CAGGCTGTCAGCTGTCTGCGCGCGCCACAGGAGGCTCGCTGCGCGCGCGCGCGCGCG 2769
 Db 901 GlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArgAlaSerGly 920
 QY 2770 GAGGGCGCTGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2829
 Db 921 GluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysValAspThrGly 940
 QY 2830 GCATCTCTCTGCTGCTGCG 2889
 Db 941 AlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThrTrpProHis 960
 QY 2890 CCTGCTGCGGGCGCTCCTCCCTCATGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2949
 Db 961 ProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProProAlaSerGln 980
 QY 2950 AGCTCCCTGCGCTGCG 3009
 Db 981 SerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSerGluProPro 1000
 QY 3010 GCCTCAGGAGCCTGCTGCTGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3069
 Db 1001 AlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProProSerGluGlu 1020
 QY 3070 GGGGTAGACTGGCG 3129
 Db 1021 GlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSerThrGlyGlu 1040
 QY 3130 CCCCACAGGCTGAGGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 3189
 Db 1041 ProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeuGluMetVal 1060

FM Modified-size 040:0.042 /note= "protein kinase C ph

CC which is a member of ERG jtkb25d10 family. This sequence is
CC from a full length clone jtkb25d10 which was derived from monkey
CC hippocampal library. ERG-LP1 is expressed exclusively in the brain.
CC Highest expression is found in cortical regions, hippocampus, caudate
CC and amygdala. The protein functions as a potassium channel modulator and
CC has neuroprotective, antiparkinsonian, anticonvulsant, antidepressant,
CC and neuroprotective, antiparkinsonian, anticonvulsant, antidepressant,

CC neuroleptic and nootropic activities. The present sequence is
CC useful for treating several potassium channel mediated disorders (CNS
CC disorders) such as Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, epilepsy, depression, schizophrenic disorders and amnesia.
XX

SQ Sequence 1083 AA;

Alignment Scores:
Pred. No.: 0 Length: 1083
Score: 5675.00 Matches: 1078
Percent Similarity: 99.63% Conservative: 1
Best Local Similarity: 99.54% Mismatches: 4
Query Match: 93.20% Indels: 0
DB: 21 Gaps: 0

US-09-965-830-1_COPY_6_3257 (1-3252) x AAY44904 (1-1083)

OY 1 ATGCGGGCCATCGGGGCTCTGCGGCTCAGAACACCTTCCTGGACACCATCGCTAGG 60
DB 1 MetProAlaMetArgGlyLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
OY 61 CGCTTCGACGGCACACAGTAACCTTCGTGGCAACGGCCAGGTGGCGGCTCTTC 120
DB 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40
OY 121 CCGTGGTCTACTGCTCTGATGGCTTCGTGACCTCAGCGGCTTCCTCGGGCTGAGTTC 180
DB 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGlnVal 60
OY 181 ATGACGGGGCTGTGCTGCTCTCTTCCTTCCTTTATGGGCGACACAGTGTGCTCGGC 240
DB 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80
OY 241 CAACAGATCCGACAGGCGCTGGACGACACAGGATTCAGGCTGAGCTGATCTGTAC 300
DB 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100
OY 301 CGGAAGCGGGCTCCGCTTCGTGTCTCTGATGTGATACCATTAAGAAATGAGAAA 360
DB 101 ArgLysSerGlyLeuProPheThrPheLysLeuLeuAspValIleProIleLysAsnGluLys 120
OY 361 GGGAGGTGGCTCTCTCTAGTCTCTCACAAAGGACATCAGCGAAGCAACAAACCGAGGG 420
DB 121 GlyGluValAlaLeuPheLeuValIserHisLysAspIleSerGluThrLysAsnArgGly 140
OY 421 GGCGCCGACAGATGGAAGGACAGAGTGTGGCGGCGCGGATATGGCGGCGACGATCC 480
DB 141 GlyProAspArgTyrLysGluThrGlySerGlyArgArgTyrGlyArgAlaArgSer 160
OY 481 AAAGGCTCAATCCACCGCGCGGCGGCGGCGGCTGTCTTACCACTGTCCGGGCAC 540
DB 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
OY 541 CTCGAAAGCAGCCCAAGGCAAGCAAGCTCAATTAAGGGGTGTGGGGAGAACCA 600
DB 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200
OY 601 AACTGCCTGAGTACAAAGTAGCGGCGCATCCGGAAGTCGCGCTTCATCCTGTGCACTGT 660
DB 201 AsnLeuProGluTyrLysValAlaIleArgLysSerProPheIleLeuLeuHisCys 220
OY 661 GGGGCACTGAGACCACTGGGATGGCTTCATCTGCTCGCCACACTTATGTGGGTGTC 720
DB 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
OY 721 ACTGTGCTACAGCTGTGTGTGACACAGCAGGAGCCAGTCCCGCCCGCGCGCG 780
DB 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
OY 781 CCAGGCTGTGTGACCTGGCGGTGGAGTCCCTTTCATCTTCACATTTGTGCTGAATTC 840
DB 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280

OY 841 CGTACCACATTCGTGTCCTCAAGTGGCGCCAGGTGGTGTTCCTCCCAAGTCCATTGGCTC 900
DB 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300
OY 901 CACTAGCTCACCACCTGCTTCCTGCTGGATGTCATCCAGCTGCTGCTTGGCTGCTA 960
DB 301 HisTyrValThrThrPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320
OY 961 CATGCTTCAAGTCAACGTACTTCGGGGCCCATCTGCTGAAGAGCGTGGCTGCTGCT 1020
DB 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340
OY 1021 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 341 ArgLeuLeuArgLeuLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360
OY 1081 ACACCTGCTCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380
OY 1141 AATGGCCAGCGGAGATCGAGACGAGCAATCCGAGTCCCTGAGATTCGCTGCTGCTGCTG 1200
DB 381 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400
OY 1201 GAGCTGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420
OY 1261 AACACCTCGGCGCAGTGCACAACTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1320
DB 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerSerSerSerSerSerSerSer 1380
OY 1321 GAGTGTGCTGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460
OY 1381 AGCAGCTCACAGCGTGGCTTTCGCGCAACGTGTCGCGCAACACACGACGACGAGATC 1440
DB 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480
OY 1441 TTCCTCATCTGCACATGCTCATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValAlaPheGlyAsnVal 500
OY 1501 ACGCCATCATCCAGCGCATGTACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 501 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520
OY 1561 CTGCGCGACTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620
DB 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540
OY 1621 TACTTCCAGGCGCCTGGCGGTGAACAATGGCATCGACACACCGAGCTGCTGCAGAGC 1680
DB 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuGlnIleSer 560
OY 1681 CTCCCTGACGAGTGGCGGACAGATCCCATGACCTGACACAGGAGGTGCTGCAGCTG 1740
DB 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580
OY 1741 CCAGTGTTCGAGCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
DB 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600
OY 1801 GCCTTTCGACGCGCGGCGGAGTACCTCATCCACCAAGCGATGCGCTGCGAGGCGCTCTAC 1860
DB 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620
OY 1861 TTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
DB 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640
OY 1921 AAGGCGCACTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980

	1001	GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProPro	1020
Db	641	LysGlyAspLeuIleGlyCysGluLeuProArgArgGluInValValLysAlaAsnAla	660
QY	1981	GACGTGAGGGGCTCACGTACTCGTCTCTGCAGTGCTTCAGCTGGCTGGCTGCACGAC	2040
Db	661	AspValLysGlyLeuThrTrpCysValLeuGlnCysLeuGlnAlaGlyLeuHisAsp	680
QY	2041	AGCCCTGCCCTGTATCCCGAGTTTCCCGGCTTCAGTCTGCTGCCCTCCGAGGGGAGCTC	2100
Db	681	SerLeuAlaLeuTyrrProGluPheAlaProArgPheSerArgGlyLeuArgGlyLeu	700
QY	2101	AGCTAACCTGGGTGCTGGGGAGGCTCTCAGAGGTGGACACCAGCTCCCTCAGGGCC	2160
Db	701	SerTyrrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly	720
QY	2161	GACATACCTTATGTCCACGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2220
Db	721	AspAsnThrLeuMetSerThrLeuGluGlnLysGluThrAspGlyGluInglyProthr	740
QY	2221	GTCTCCCCAGCCCAGCTCATGAGCCCTCCAGCCCTCTGCTGCTCCCTGCTGCACTCC	2280
Db	741	ValSerProAlaProAlaaspGluProSerSerProLeuLeuSerProGlyCysThrSer	760
QY	2281	TCTATCTCAGCTGCCAAGCTGTATCCACGCTGTAACAGCAGCAGCCCGCTCTAGGT	2340
Db	761	SerSerSerAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly	780
QY	2341	GGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2400
Db	781	GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro	800
QY	2401	CCAGGGGCTTAGAGGGCTAGCGCTGCCCCCAGCTGCCATGGAATGCTCCCGCAGATCG	2460
Db	801	ProArgAlaLeuGluGlyLeuArgLeuProPrometProTrpAsnValProProaspLeu	820
QY	2461	AGCCCCAGGTACTAGTGCATTGAAGAGCGGTGGCTCGGACAGCCAAAGTTCTCT	2520
Db	821	SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer	840
QY	2521	TTCCGCTGGCCGAGTCTGCCCGGAATGTAGCAGCAGCCCTCCCTGGACGAGAGC	2580
Db	841	PheArgMetGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer	860
QY	2581	GGCTGCTCACTGTCCCATGGGCCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2640
Db	861	GlyLeuLeuthrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys	880
QY	2641	CTTCGGAGGGGTGACAGAGCTGTACAGCAGGCTCTCAGATGGGGAAGGAGCTGCAG	2700
Db	881	LeuArgGlnAlaValMetGluLeuSerGluInValLeuGlnMetArgGlyLeuGln	900
QY	2701	TCATCTGCCAGGTGTGAGCTGTCTGCGCCGCCACAGGAGGAGGAGGAGGAGGAGGAGG	2760
Db	901	SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg	920
QY	2761	GCATCGGAGAGGGGCGTGCACAGCAGCAGCTCCGGGCTTCGAGGCTCTGTGTGTG	2820
Db	921	AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuGlyVal	940
QY	2821	GACACTGGGGCATCTCTACTGTGCTGAGCCGCCAGCTGGCTCTCTGTAGTGGGACT	2880
Db	941	AspThrGlyAlaSerSerTyrrCysLeuGlnProProAlaGlySerValLeuSerGlyThr	960
QY	2881	TGGCCCCACCTCTGTCGGGGGCTCTCCCTCATGACACCCCTGGGCTGGGTCGCCCA	2940
Db	961	TrpProHisProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProPro	980
QY	2941	GGCTCTAGACTCCCTGCTGAGCCAGCAGCTTCTGGACCTCCACCTCAGACTCA	3000
Db	981	AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerAspSer	1000
QY	3001	GAGCCCCCTGCTCAGGAGACTCTGTCTGAGCCAGCAGCCCTGCTCCCTCTCTCTCT	3060

QY	1801	GCCTTCTGCACGCGCGCGGAGTACCTCATCACCAAGCGAGTCCCTGCAGGCCCTCTAC	1860
DB	600	AlaPheCysThrProGlyGluTyLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTy	619
QY	1861	TTTCTGTGCTTGTGCTCCATGAGGAGGTGCTAAGGGTGCACCGTGCCTGCCATCTAGGG	1920
DB	620	PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly	639
QY	1921	AAGGGCAGCTGATCGCTGTGAGTCCCGCGGGGAGCAGGTGGTAAAGGCCAATGCC	1980
DB	640	LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla	659
QY	1981	GACGTGAAGGGCTGACGTACTCGCTGCTGCAGTGTCTGCAGCTGCCTGCGCTGCACGAC	2040
DB	660	AspValLysGlyLeuThrTyCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisasp	679
QY	2041	AGCCTTGCCTGTACCCCGAGTTTCCCGCGGCTTCACTCTGTGCGCTCCGAGGGAGCTC	2100
DB	680	SerLeuAlaLeuTyProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu	699
QY	2101	AGCTACACCTGGGTGTGGGGAGGTCTGCAGAGTGGACACAGTCCCTGAGCGGC	2160
DB	700	SerTyAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly	719
QY	2161	GACAAATACCTTATGTCACGCTGGAGGAGAGGAGACAGATGGGAGCAGGGCCCCCAGC	2220
DB	720	AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr	739
QY	2221	GTCCTCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGCTCCCTGGCTGCACCTCC	2280
DB	740	ValSerProAlaProAlaAspGluProSerProLeuLeuSerProGlyCysThrSer	759
QY	2281	TCATCCTCAGCTGCCAAGCTGTATCCCACTGCAAGACAGCACCCGGCTCGTCTAGGT	2340
DB	760	SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly	779
QY	2341	GGCAGAGGAGGCCAGGCGAGGCGCTTTGAAGCTGAGGCTGGCCCTGCTCTCTCC	2400
DB	780	GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro	799
QY	2401	CCACGGGCGCTAGAGGGGTACGGCTGCCCGCCCATGCCATGCAATGAAATGCCCCCAGATCTG	2460
DB	800	ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu	819
QY	2461	ACCCCCAGGTAGTAGTGGCATTAAGAGCGCTGGCTCGACCGACCGCCAAGTTCTCT	2520
DB	820	SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer	839
QY	2521	TTTCCGGTGGGCGAGTCTGGCCGGAATATGACAGCAGCGCCCTCCCTGCACAGAGAGC	2580
DB	840	PheArgValLysGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer	859
QY	2581	GGCTGTCTCACTTCTCCCATGGGCCACGAGGCAAGGAACACACACACTGGACAAG	2640
DB	860	GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys	879
QY	2641	CTTGGCAGGCGGTACAGAGTGTCCAGACAGGTGCTGCAGATGGCGGGAAGACTGTCAG	2700
DB	880	LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln	899
QY	2701	TCATTCGCCAGCTGTGAGCTTGTCTTCTGGGCCCCCAGAGGAGGTCCGTCGCCCTCGG	2760
DB	900	SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg	919
QY	2761	GCATCGGGAGAGGGCGGTGCCAGCACCTCCGGGCTTCTGCAGGCTCTGTGTGTG	2820
DB	920	AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal	939
QY	2821	GACACTGGGCGATCCCTACTGCCTGCAGCCCCCAGCTGGCTGTCTTGTAGTGGGACT	2880
DB	940	AspThrGlyAlaSerSerTyCysLeuGlnProProAlaGlySerValLeuSerGlyThr	959
QY	2881	TGSCCCCCACCTCTGTCGGGGCGCTCTCCCTCATGGCACCTCGGCCCTGGGTGCCCCA	2940

Db	960	TrpProHisProArgProGlyProProProLeuMetAlaProArgProTrpGlyProPro	979
Qy	2941	GCCTCTCAGAGCTCCCTGGCTCGAGCCACACAGCTTTCTGGACCTCCACCTCAGACTCA	3000
Db	980	AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer	999
Qy	3001	GAGCCCTCCCTCAGAGAGACCTCTGCTGTGAGCCACCCAGACCCCTGCCCTCCTCCTCT	3060
Db	1000	GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro	1019
Qy	3061	TCCTGAGGAAGGGCTAGGACTGGCCCGCAGACCCCTGTGAGCAGCTCAGCTCAGCTAC	3120
Db	1020	SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer	1039
Qy	3121	ACTGAGAGCCCCACACAGGTCAGGGGCTCGCTTGGCTTGGCTGGACCCACCCACACCTG	3180
Db	1040	ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu	1059
Qy	3181	GAGATGTGCTTATTGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGC	3240
Db	1060	GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGluGly	1079
Qy	3241	ACAGGGGTC	3249
Db	1080	ThrGlyVal	1082
RESULT	l0		
AA	AY44907		
ID	AA44907	standard; Protein; l107 AA.	
XX	AA44907;		
XX			
DT	18-MAY-2000	(first entry)	
XX			
DE	Human potassium channel molecule ERG-LP2 full-length protein.		
XX			
KW	Human; potassium channel molecule; ERG-like protein 2; ERG-LP2;		
KW	neuroprotective; antiparkinsonian; anticonvulsant; antidepressant;		
KW	neuroleptic; nootropic; treatment; CNS disorder; central nervous system;		
KW	potassium channel mediated disorder; epilepsy; Alzheimer's disease;		
KW	Parkinson's; multiple sclerosis; depression; schizophrenia; amnesia;		
KW	chromosome 3p21.3-24.3.		
XX			
OS	Homo sapiens.		
XX			
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FT	Modified-site	953	
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FT	Modified-site	63..65	
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FT		/note= "Protein kinase C phosphorylation site"	
FT	Modified-site	159..161	
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FT	Modified-site	216..218	

FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	250..252
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	329..331
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	413..415
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	616..618
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	683..685
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	733..735
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	741..743
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	749..751
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	771..773
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	807..809
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	830..832
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	1078..1080
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	10..13
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	17..20
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
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FT	Modified-site	547..550
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FT	Modified-site	616..619
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	624..627
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	632..635
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FT	Modified-site	689..692
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
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FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	819..822
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	1033..1036
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
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FT	Modified-site	161..164
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PN	W0200005346-A1.	
PD	03-FEB-2000.	
XX		
XX		

21-JUL-1999; 99WO-US16752.
 21-JUL-1998; 98US-0119855.
 (MILL-) MILLENNIUM PHARM INC.
 Curtis RAJ;
 WPI: 2000-182682/16.
 N-PSDB; AAZ50455.
 Novel gene encoding potassium channel molecule useful in treating central nervous system disorders such as Alzheimer's disease, multiple sclerosis, and schizophrenia
 Example 1; Fig 8; 144pp; English.
 The present sequence is a full-length ERG-like protein 2 (ERG-LP2) which is a member of ERG potassium channel family. This sequence is a result of additional sequencing of clone jlhbaa042h05 which was obtained from human brain library. ERG-LP2 gene is mapped to human chromosome 3p21.3-24.3, between markers WI-4218 and RP-L1S_1. It is predominantly expressed in the brain.
 The protein functions as a potassium channel modulator and has neuroprotective, antiParkinsonian, anticonvulsant, antidepressant, neuroleptic and nootropic activities. The present sequence is useful for treating several potassium channel mediated disorders (CNS disorders) such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, epilepsy, depression, schizophrenic disorders and amnesia.

FF 21-JUL-1999; 99WO-US16752.
 XX
 PR 21-JUL-1998; 98US-0119855.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Curtis RAJ;
 XX
 DR WPI: 2000-182682/16.
 DR N-PSDB; AAZ50455.
 XX
 PT Novel gene encoding potassium channel molecule useful in treating
 PT central nervous system disorders such as Alzheimer's disease, multiple
 PT sclerosis, and schizophrenia
 PS Example 1; Fig 8; 144pp; English.
 XX
 CC The present sequence is a full-length ERG-like protein 2
 CC (ERG-LP2) which is a member of ERG potassium channel family. This
 CC sequence is a result of additional sequencing of clone jlhbaa042h05 which
 CC was obtained from human brain library. ERG-LP2 gene is mapped to
 CC human chromosome 3p21.3-24.3, between markers WI-4218 and RP-L1S_1. It
 CC is predominantly expressed in the brain.
 CC The protein functions as a potassium channel modulator and
 CC has neuroprotective, antiParkinsonian, anticonvulsant, antidepressant,
 CC neuroleptic and nootropic activities. The present sequence is
 CC useful for treating several potassium channel mediated disorders (CNS
 CC disorders) such as Alzheimer's disease, Parkinson's disease, multiple
 CC sclerosis, epilepsy, depression, schizophrenic disorders and amnesia.
 XX
 SQ Sequence 1107 AA;

Alignment Scores:
 Pred. No.: 1.74e-156 Length: 1107
 Score: 2529.50 Matches: 559
 Percent Similarity: 60.24% Conservative: 150
 Best Local Similarity: 47.49% Mismatches: 267
 Query Match: 41.54% Indels: 201
 DB: Gaps: 27
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 Db 21 ArgPheaspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40
 QY 121 CCCGTGTCTACTGCTCTGTAGTGGCTTCTGTACCTCAGCGGCTTCTCCCGGGCTGAGTC 180
 Db 41 ProtleValTyrCysSerAspGlyPheCysgluLeuAlaGlyPheAlaArgThrGluVal 60
 QY 181 ATGACGGGGGCTGCTGCTGCTCTCTTTATGGCCAGACACAGTAGCTCGTCCGC 240
 Db 61 MetGlnLysSerCysSerLysPheLeuPheGlyValGluThrAsnGluLeuMet 80
 QY 241 CAACAGATCCGACAGGCCCTGGACGACACAAAGGATTCAAGGCTGAGCTGATCCTGTAC 300
 Db 81 LeuGlnileGluLysSerLeuGluclLysThrGluPheLysGlyGluileMetPheTyr 100
 QY 301 CGGAAGACGGGCTCCCGTCTGCTGCTGCTGCTGATGTATACCATAAAGAATGAGAAA 360
 Db 101 LysLysasnGlySerProPheTrpCysLeuLeuAspileValProIleLysAsnGluLys 120
 QY 361 GGGAGGTGGCTCTCTTCCTAGTCTCTCAACAAGACATCAGCGAACAACAGACCGAGG 420
 Db 121 GlyAspValvalLeuPheLeuAlaSerPheLysAspileThrAspThrLysVallysile 140
 QY 421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCCGCGATATGCCCGGGGACGATCC 480
 Db 141 ThrProgluasplysLysGluAsp-----LysVallysGlyArgSerArqAla 156
 XX
 XX

QY	481	---	AAAGGCTTCAATGCCAACCGCGCGGAGCGCGGCTGTCTACACACCTGCTCGGG	537
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Db	177	HisLeuGlnArgArgGluLysAsnLysLeuLysIleAsnAsnValPheValAspLys	196	
QY	598	CCAAACTGGCTGAGTACAAAGTAGCGCCATCCGGAGTCGCCCTTCATCTGTTGCAC	657	
Db	197	ProAlaPheProGluTyrLysValSerAspAlaLysSerLysPheIleLeuLeuHis	216	
QY	658	TGTGGGCACTGAGAGCCACTGGATGGCTTCATCTGCTGCGCACACTCTATGTGGCT	717	
Db	217	PheSerThrPheLysAlaGlyTrpAspTrpLeuIleLeuAlaThrPheTyrValAla	236	
QY	718	GTCACCTGTCCTACAGCGTGTGTGAGCACACAGCGGAGCCAGTGGCGCGCGG	777	
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QY	778	CCGCCACGCTGTGACCTGGCGGTGAGGTCTCTTCATCTTCATCTGCTGCTGAT	837	
Db	257	---ThrThrValSerAspIleAlaValGluIleLeuPheIleIleAspIleIleLeuAsn	275	
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Db	316	LeuTyrAlaPheAsnValThrValVal1SerLeuValHisLeuLeuLysThrValArgLeu	335	
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QY	1258	GGGAACAGCTCCGGCCAGAGTACAACTGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1317	
Db	408	GlyAsnAsnThr	411	
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QY	1498	GTGACGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACACAGCCGCGCGC	1557	
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QY 2662 CTGTGAGCAGCGTGTGAGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2721
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RESULT 11
AA83028
ID AA83028 standard; Protein; 1102 AA.
XX
AC AA83028;
XX
DT 04-JUL-2000 (first entry)
XX
DE Rat Elk1 potassium channel protein.
XX
KW Elk1; elk2; eag1; eag2; erg1; potassium channel; membrane protein;
KW drug screening; hypertension; renal failure; diabetes insipidus;
KW diabetic nephropathy; hypothyroidism; goiter; hypoparathyroidism;
KW pancreatic insufficiency; diabetes mellitus; cystic fibrosis;
```

```
KW sialorrhea; salivary insufficiency; membrane potential; current flow;
KW ion flux; transcription; signal transduction; assay; detection;
KW rat.
OS Rattus rattus.
XX
PN WO200012546-A1.
XX
PD 09-MAR-2000.
XX
PF 31-AUG-1999; 99WO-US19902.
XX
PR 31-AUG-1998; 98US-0098413.
XX
PA (UUNY ) UNIV NEW YORK STATE RES FOUND.
XX
PI McKinnon D, Dixon JB;
XX
DR WPI; 2000-256585/22.
XX
DR N-PSDB; AA293334.
XX
Novel mammalian potassium channel genes and polypeptides encoded by
them for screening drugs useful for treating diseases such as
hypertension, acute renal failure, diabetes insipidus and
hypothyroidism -
Claim 29; Page 82-86; 102pp; English.
XX
Potassium channel genes e.g. elk1, elk2 or eag2 are useful for
identifying modulators which are useful for treating hypertension,
acute and chronic renal failure, diabetes insipidus, diabetic
nephropathy, hyperthyroidism, goiter, hyperparathyroidism,
pancreatic insufficiency, diabetes mellitus, cystic fibrosis,
sialorrhea, salivary insufficiency. The availability of the gene
sequences provides a tool for research into the physiological
characteristics of the various genes and proteins for potassium
channels including the development of medicines effective for
treating disease conditions associated with mutations or defects in
potassium channels and the screening of drugs to ensure that
potassium channels are not blocked or physiologically affected by
those drugs. The channel proteins encoded by these genes are also
useful themselves as reporter molecules in assay and detection
systems to measure changes in potassium concentration, membrane
potential, current flow, ion flux, transcription, signal
transduction, receptor-ligand interaction and second messenger
concentrations.
XX
SQ Sequence 1102 AA;
Alignment Scores:
Pred. No.: 1,53e-155 Length: 1102
Score: 2515.00 Matches: 551
Percent Similarity: 62.00% Conservative: 149
Best Local Similarity: 48.80% Mismatches: 295
Query Match: 41.30% Indels: 134
DB: 24
Gaps: 24
US-09-965-830-1_COPY_6_3257 (1-3252) x AA83028 (1-1102)
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Db 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTCGACGCGCAGCAGTAACTTGTGTGGGCAAGCCCGAGGTGGCGGCTCTTC 120
Db 21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaGlnValAlaLysGlyPhe 40
QY 121 CCCGTGTCTACTCTCTGATGGCTTCTGTACCTCAGCGGCTTCTCCCGGCTGAGGTC 180
Db 41 ProIleValTyrCysSerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluVal 60
QY 181 ATGACGCGGCGCTGCTGCTCTCTCTTATGGCGCAGACCATGACCTGCTGTCGC 240
Db 181 ATGACGCGGCGCTGCTGCTCTCTCTTATGGCGCAGACCATGACCTGCTGTCGC 240
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Db 61 MetGlnLysSerCysSerCysLysPheLeuPheGlyValGluThrAsnGluGlnLeuMet 80
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 Db 81 LeuGlnIleGluLysSerLeuGluGlnLysValGluPheLysGlyGluIleMetPheTyr 100
 Qy 301 CGGAAGAGGGGCTCCGCTTCCTGGTGTCTCCCTGATGATACCCATAAAGAAATGAGAAA 360
 Db 101 LysLysAsnGlyAlaProPheTrpCysLeuLeuAspIleValProIleLysAsnGluLys 120
 Qy 361 GGGAGGTGGCT 417
 Db 121 GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 140
 Qy 418 GGGGGCCCCACAGATGGAAGAGACAGGTGTGTGGCGCGCGATATGGCGGGCACGA 477
 Db 141 ThrSerGluAspLysLysGluAspArgAlaLysGlyArgSerArgAlaGly----- 157
 Qy 478 TCCAAAGGCTTCAATCCCAACGGCGCGAGCGCGCGTGTCTTACACCTGTCCGGG 537
 Db 158 ---SerHisPheAspSerAlaArgArgSerArgAlaValLeuTyrHisIleSerGly 176
 Qy 538 CACCTCACAAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTGTGGGAGAAA 597
 Db 177 HisLeuGlnArgArgGluLysAsnLysLysLysLysLysLysLysLysLysLysLys 196
 Qy 598 CCAAACTTCCTGAGTACAAAGTAGCCGCATCCGGAAGTGCCTCTCATCTCTGTTCAC 657
 Db 197 ProAlaPheProGluLysValSerAspAlaLysLysSerLysPheIleLeuLeuHis 216
 Qy 658 TGTGGGCACTGAGACCCAGCTGGATGCTCATCTCTCTCTCTCTCTCTCTCTCTCTCT 717
 Db 217 PheSerThrPheLysAlaGlyTrpAspTrpLeuIleLeuLeuAlaThrPheTyrValAla 236
 Qy 718 GTCACTGTCCCTACAGCTGTGTGTGAGCAGCAGCGGAGCCAGTGCCTCCCGCGG 777
 Db 237 ValThrValProTyrAsnValCysPheIleGlyAsnLysPheSerThrThrArgSer 256
 Qy 778 CCGCCAGCTGTGTGACCTGCGCGGTGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 837
 Db 257 ---ThrThrValSerAspIleAlaValGluIlePheIleIleAspIleIleLeuAsn 275
 Qy 838 TTCCTGACACATCTGT 897
 Db 276 PheArgThrThrTyrValSerLysSerGlyGlnValIlePheGluAlaArgSerIleCys 295
 Qy 898 CTCACCTACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957
 Db 296 IleHisTyrValThrThrTrpPheIleIleAspLeuIleAlaLeuProPheAspLeu 315
 Qy 958 CTACATCCCTCAAGTCAACGTGTACTTCCGGGCGCATCTGTGAGACGGTGCCTG 1017
 Db 316 LeuTyrAlaPheAsnValThrValValSerLeuValHisLeuLysThrValArgLeu 335
 Qy 1018 CTGGCTGTGTGCTGT 1077
 Db 336 LeuArgLeuLeuArgLeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleVal 355
 Qy 1078 CTGACACTGTCTATGGCGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1137
 Db 356 LeuThrLeuLeuMetSerMetPheAlaLeuAlaHisTrpMetAlaCysIleTrpTyr 375
 Qy 1138 TACATTGGCAGCGGGATGAG 1197
 Db 376 ValIleGlyLysMetGluArgGluAspAsnSerLeuLeuLysTrpGluValGlyTrpLeu 395
 Qy 1198 CAGGAGTGGCCCCCTGAGACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1257
 Db 396 HisGluLeuGlyLysArgLeuGluSerProTyr----- 407
 Qy 1258 GGAACAGCTCCGGCCAGAGTGACAACTGACGAGCAGCAGGAGGAGGAGGAGGAGGAG 1317
 Db 408 GlyAsnAsnThr----- 411

Qy 1318 CTGGAGCTCTCTGGGGCGCGCTGCTGCGCAGCGCTACATCACCTCCCTCTACTTCGCA 1377
 Db 412 -----LeuGlyGlyProSerIleArgSerAlaTyrIleAlaAlaLeuTyrPheThr 428
 Qy 1378 CTCACGAGCTCACCAGCGTGGCTTCCGCAACGCTGCTCGCCCAACACGACACCGAGAAG 1437
 Db 429 LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLys 448
 Qy 1438 ATCTCTCTCATCTGCACCATCTGCTGCGCGCTGATGCAGCGGTGTGTGTGGGAAC 1497
 Db 449 IlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaLeuValPheGlyAsn 468
 Qy 1498 GTACGCGCATCATCAGCGCATGTACGCGCGCTTCTGTACACAGCCGACGCGCGC 1557
 Db 469 ValThrAlaIleIleGlnArgMetTyrSerArgTrpSerLeuTyrHisThrArgThrLys 488
 Qy 1558 GACCTCGCGACTACATCCGATCCACCTGATATCCCAAGCCCTCAAGCAGCCGCTGCTG 1617
 Db 489 AspLeuLysAspPheIleArgValHisHisLeuProGlnGlnLeuLysGlnArgMetLeu 508
 Qy 1618 GAGTACTTCCAGCCACCTGGCGGTGAACATGGCATCGACACACCGAGCTGTGCAG 1677
 Db 509 GluTyrPheGlnThrThrTrpSerValAsnAsnGlyIleAspSerAsnGluLeuLeuLys 528
 Qy 1678 AGCTCCCTGACGAGTGGCGCAGATCGCCATCGCATCGACACACCGAGCTGTGCAG 1737
 Db 529 AspPheProAspGluLeuArgSerAspIleThrMetHisLeuAsnLysGluIleLeuGln 548
 Qy 1738 CTCCCTACTGTTGAGCGGCGACCGCGCTGCTGCGGCACTGTCTGTGGCCCTGCGG 1797
 Db 549 LeuSerLeuPheGluCysAlaSerArgGlyCysLeuArgSerLeuSerLeuHisIleLys 568
 Qy 1798 CCGCCCTTGTGACGCGCGGAGTACCTCATCCCAAGCGCATGCCCTGCGAGGCCCTC 1857
 Db 569 ThrSerPheCysAlaProGlyGluTyrLeuLeuArgGlnGlyAspAlaLeuGlnAlaIle 588
 Qy 1858 TACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1917
 Db 589 TyrPheValCysSerGlySerMetGluValLeuLysAspSerMetValLeuAlaIleLeu 608
 Qy 1918 GGAAGGCGCACCTGATCGCTGTGAGTCCCGCGGAGGAGGAGTGTGTAAGGCCAAT 1977
 Db 609 GlyLysLysAspLeuIleGlyAlaAsnLeuSerIleLysAspGlnValIleLysThrAsn 628
 Qy 1978 GCGCACGTGAAGGGCTGACGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2037
 Db 629 AlaAspValLysAlaLeuThrTyrCysAspLeuGlnCysIleIleLeuLysGlyLeuPhe 648
 Qy 2038 GACAGCTTGGCTGTACCGGAGTTGCGCGGCTTACGCTGCTGCTGCTGCTGCTGCTGCT 2097
 Db 649 GluValLeuGlyLeuTyrProGluTyrAlaHisLysPheValGluAspIleGlnHisAsp 668
 Qy 2098 CTCAGCTACAACTGGTGTGCTGG-----GGAGGCTCT 2130
 Db 669 LeuThrTyrAsnLeuArgGluGlyHisGluSerAspValIleSerArgLeuSerAsnLys 688
 Qy 2131 GCAGAGTGGACACAGCTCCCTGAGCGGCGACAATACCTTATGTCACACCTG----- 2184
 Db 689 SerThrValProGlnAlaGluProLysGlyAsnGlySerIleLysLysArgLeuProSer 708
 Qy 2185 -----GAGGAGAGGAGACAGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2235
 Db 709 IleValGluAspGluGluGluGluValGluGluGluGluGluGluGluGluGluGlu 728
 Qy 2236 GCTGATGAGCCCTCAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2295
 Db 729 IleTyrThrArgGlySerValSerHisSerLysLysThrGlySerSerLysSerTyr 748
 Qy 2296 AAGTGTATATCCCAAGCTGCA-----ACAGCACCC-----CGCT 2334
 Db 749 LeuGlyLeuSerLeuLysGlnLeuThrSerGlyThrValProPheHisSerProIleArg 768

121 GlyGluValValLeuPheLeuPheSerPheLysAspIleThrClnSerGlySerProGly 140
141 LeuGlyProGln-----GlyGlyArgGlyAspSerAsnHisGluAsn 154
478 TCAAAAGGC-----TTCATGCCAACCGGGGGGGGGGGCC 516
155 SerLeuGlyArgArgGlyAlaThrTrpLysPheArgSerAlaArgArgSerArgThr 174
517 GTGCTCTACACCTGTCGGGACCTGCAGAACGCCCAAGGCAAGCAGCTCAAT 576
175 ValLeuHisArgLeuThrGlyHisPheGlyArgGlyGlnGlyMetLysAlaAsn 194
577 AAGGGGTGTTGGGAGAAACCAACTTCCTGAGTACAAAGTAGCCGCTCCGGAAG 636
195 AsnAsnValPheGluProLysProSerValProGluTyrLysValAlaSerValGlyGly 214
637 TGGCCCTTCATCTGCTGTCAGTGGGCACTGAGAGCACCTGGGATGGCTTCATCTG 696
215 SerArgCysLeuLeuHisTyrSerValSerLysAlaIleTrpAspGlyLeuLeu 234
697 CTGCGCACACTATGCTGCTGTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 756
235 LeuAlaThrPheTyrValAlaValThrValProTyrAsnValCysPheSerGlyAsp 254
757 GAGCCAGTCCG 816
255 AspThrProIleThrSerArgHisThrLeuValSerAspIleAlaValGluMetLeuPhe 274
817 ATCTCTGACATTCGCTGAATTCCTGACACATTCGCTGCTGCTGCTGCTGCTGCTG 876
275 IleLeuAspIleLeuLeuAsnPheArgThrThrThrValSerGlnSerGlyGlnVal 294
877 TTTGCCCAAGTCCATTTGCCCTCCTAGTACACCTGCTGCTGCTGCTGCTGCTGCTG 936
295 SerAlaProArgSerIleGlyLeuHisTyrLeuAlaThrTrpPheIleAspLeuLe 314
937 GCAGCGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 996
315 AlaAlaLeuProPheAspLeuLeuTyrIlePheAsnIleThrValThrSerLeuValHis 334
997 CTGCTGAAGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1056
335 LeuLeuLysThrValArgLeuLeuArgLeuLeuArgLeuLeuLysLeuValArgTyr 354
1057 TCCAGTACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1116
355 SerGlnCysSerAlaValValLeuThrLeuThrLeuMetSerValPheAlaLeuLeuAlaHis 374
1117 TGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1176
375 TrpMetAlaCysIleTrpTyrValIleGlyArgGluMetGluAlaAsnAspProLeu 394
1177 CTGCTGAGATTGGTGGTGCAGAGAGTGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTG 1236
395 LeuTrpAspIleGlyTrpLeuHisGluLeuGlyLysArgLeuGluValProTyr----- 412
1237 GTGGCGGAGCGCAGCTGGAGGAGACAGCTCCGCGCCAGAGTGCACACTGCAGCAGCAGC 1296
412 -----ValAsnGlySer-----ValGlyProSerArgSerAlaTyr 426
1297 AGCAGGCCAACGGGAGCGGCTGGAGCTGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCT 1356
413 -----ValAsnGlySer-----ValGlyProSerArgSerAlaTyr 426
1357 ATCACTCTCTACTTCGCACTCAGCAGCTCACCAGCTGGGCTTCGCAAGCTGCTC 1416
427 IleAlaAlaLeuTyrPheThrLeuSerSerLeuThrSerValGlyPheGlyAsnValCys 446
1417 GCCAACGAGCAGCGAGAGATCTTCTCATCTGTCACCATGCTCATCGCGCGCTGATG 1476

447 AlaAsnThrAspAlaGluLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMet 466
1477 CAGCGGTGTGTTGGGAACGTGACGGCATCATCCAGCGCATGACGGCCGCGCTTT 1536
467 HisAlaValValPheGlyAsnValThrAlaIleIleGlnArgMetTyrSerArgSer 486
1537 CTGTACACAGCGCGACCGACCTCGCGCTACATCCGATCCACCGTATCCCAAG 1596
487 LeuTyrHisSerArgMetLysAspLeuLysAspPheIleArgValHisArgLeuProArg 506
1597 CCCTCAACAGCGCATGCTGGAGTACTTCCAGGCCACCTGGCGGTGAAATGCGCATC 1656
507 ProLeuLysGlnArgMetLeuGluTyrPheGlnThrTrpAlaValAsnSerGlyIle 526
1657 GACACACAGCGTGTGTCAGAGCTCCCTGAGAGCTGCGCGCAGACATCGCCATGCCAC 1716
527 AspAlaAsnGluLeuLeuArgAspPheProAspGluLeuArgAlaAspIleAlaMetHis 546
1717 CTGCACAAGGAGTCTGTCAGCTGCCACTCTTGGAGCGCGCGCGCTGCTGCTGCTGCGG 1776
547 LeuAsnArgGluLeuLeuGlnLeuProLeuPheGlyAlaAlaSerArgGlyCysLeuArg 566
1777 GCAGTCTCTGCGCTGCGCGCGCGCTTCTGCACGCGCGCGCGCTACCTATCCACCAA 1836
567 AlaLeuSerLeuHisIleLysThrSerPheCysAlaProGlyGluTyrLeuLeuArgArg 586
1837 GCGAGTCCCTGCGAGCGCTCTACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1896
587 GlyAspAlaLeuGlnAlaHisTyrTyrValCysSerGlySerLeuGluValLeuArgAsp 606
1897 GGCACCGTGTCTGCCATCTCCTAGGAAAGCGGCTGATGCTGCTGCTGCTGCTGCTGCTG 1956
607 AsnMetValLeuAlaIleLeuGlyLysGlyAspLeuIleGlyAlaAspIleProGluPro 626
1957 GAGCAG-----GTGTAAGGCCATGCGGAGTG 1986
627 GlyGlnGluProGlyLeuGlyAlaAspProAsnPheValLeuLysThrSerAlaAspVal 646
1987 AAGGGCTGACGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2046
647 LysAlaLeuThrTyrCysGlyLeuGlnLeuSerSerArgGlyLeuAlaGluValLeu 666
2047 GCGTGTACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2106
667 ArgLeuTyrProGluTyrGlyAlaAlaPheArgAlaGlyLeuProArgAspLeuThrPhe 686
2107 AACCTGGTCTGCGGAGGCTCTGAGAGGTGGACACACAGCTGCTGCTGCTGCTGCTGCTG 2154
687 AsnLeuArgGlnGlySer-----AspThrSerGlyLeuSerArgPheSer 701
2155 -----ACGGCGCAATACC 2169
702 ArgSerProArgLeuSerGlnProArgSerGluSerLeuGlySerSerSerSerLysThr 721
2170 CTATGCTCCAGCTGGAGAGAGAGACAGATGGGAGAGCGGCGCGCGCGCTGCTGCTGCTGCT 2229
722 LeuProSerIle-----ThrGluAlaGluSerGly-----AlaGluPro 734
2230 GCGCCAGCTGATGAGCCCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2289
735 GlyGlyGlyProArgProArgArgProLeuLeuProAsnLeuSerProAlaArgPro 754
2290 GCTGCCAAGCTG----- 2301
755 ArgGlySerLeuValSerLeuLeuGlyGluLeuProPheSerAlaLeuValSer 774
2302 -----CTATCCCGCAGCTCGAACAGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2352
775 SerProSerLeuSerProSerLeuSer-----ProAlaLeuAlaGlyGlnGlyHis 791
2353 CCAGCGAGCGCGGCTTTCAAGGCTGAGGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2412
792 -----SerAlaSerProHisGlyProProArgCysSer 802

QY	2413	GAGGGG-----CTACGGCGTGCCTCCCATGCCATGGAAATGTGCCCCCAGAT	2457
Db	803	AlaAatrlPlysProProGlnLeuLeuIleProProLeuGlyThrPheGlyProProAsp	822
QY	2458	CTGAGCCCCAGGTAGTAGTCATTGAAGAC---GGCTGTGGCTCGGACCCAGC	2514
Db	823	LeuSerProArgIleValAspGlyIleGlusSergGlySerThrAlaGluAlaProSer	842
QY	2515	TTCCTCTTTCCGCTGGGCCAGTCTGGCCCCGGAATGTAGCAGCACGCCCTCCCTTG	2574
Db	843	PheArgPhe-----SerArgProGluLeuProArgProArgSerGlnAlaPro	859
QY	2575	GAGAGCGGCGTCTCACTGTTCGCCATGGGCCCCAGCAGCAGCAAGAACACA---	2631
Db	860	ProThrGlyThrArgProSerProGluLeuAlaSerGluAlaGluValLysGluLys	879
QY	2632	CTGGACAAGCTTGGCAGCGGTCACAGACTGTACAGCAGAGTGTCTGCAGATCGCG	2691
Db	880	ValCysArgLeuAsnGlnGluIleSerArgLeuAsnGlnGluValSerGlnLeu-Ser	899
QY	2692	GGACTCAGTCACTTCGCCAGGCTGTGCAGCTGTCTGGCGCCCCACAGGGAGGTC	2751
Db	899	GluLeuArgHisIleMetGlyLeuLeu-----	908
QY	2752	TGCCCTCGGGCATCGGGAGAGGGCGCTGCCAGCCAGCACCCTCCGGGCTTCGCAC	2811
Db	909	-----GlnAlaArgLeuGlyProPro-----	915
QY	2812	CTGTGTGTGGACACTGGGCATCTCTACTGCTGCAGCCCCCAGCTGCTGTCTGT	2871
Db	916	-----GlyHisProAlaGlySer-----	921
QY	2872	AGTGGACTTGGCCCCACCCTCGTCGGGGCGCTCCCTCATGTGCACCCCTGGCCCT	2931
Db	922	-----AlaTipThrProAspProPr	928
QY	2932	GGTCCCGCCAGCGTCTCAGAGCTCCCGCTGGCTCGAGCCACAGCTTCTGGACCT	2991
Db	928	cCysProGln-----LeuArg---ProProcysLeuSerProCysAlaSerArg	946
QY	2992	TCAGACTCAGAGC-----	3004
Db	946	oSerLeuGlnAspThrThrLeuAlaGluValHIScysProAlaSerValGlyThr	966
QY	3005	-----CCCTCGCTCAGGAGAC	3021
Db	966	uThrGlyThrAlaLeuAlaLeuAspLeuArgProSerIleLeuProTytyrProSer	986
QY	3022	CTCTGCTCTGAGCCAGCACCCTGCCT	3049
Db	986	oAspProLeuGlyProSerProValPro	995
RESULT	13		
AAY	77739		
ID	AAY77739	standard; Protein; 457 AA.	
XX			
AC	AAY77739;		
XX			
DT	19-MAY-2000	(first entry)	
XX			
DE	Human ESK1 (hESK1) protein fragment (residues 212-668).		
XX			
KW	ESK1; eag similar K+ channel; potassium channel associated disorder;		
KW	neurological; Alzheimer's disease; anxiety; panic; autism; hyperactivity;		
KW	obsessive-compulsive disorder; schizophrenia; Huntington's disease;		
KW	epilepsy; cardiovascular; musculoskeletal; proliferative; cancer;		
KW	ESK channel blocker; nootropic; neuroprotective; antidepressant;		
KW	tranquillizer; neuroleptic; antiParkinsonian; cardiant; cytostatic;		
KW	anticongulsant.		
OS	Homo sapiens.		
XX			

QY	1063	TACAGCGCGTGTGCTGACACTGCTCATGGCGGTTCGCCCTGCTCGCGCACTGGGTC	1122
Db	141	TyrSerAlaValLeuThrLeuMetAlaValPheAlaLeuAlaHisTrpVal	160
QY	1123	GCTGCGTCTGTTTACATGGCCAGCGGAGATCGAGAGCGAATCCGAGCTGCCT	1182
Db	161	AlaCysValTrpPheTyrIleGlyGlnArgGluLeuSerSerGluLeuPro	180
QY	1183	GAGATTGGCTGGCTGACAGAGTGGCCCGGCTGAGACTCCCTACTACCTGGTGGC	1242
Db	181	GluIleGlyTrpLeuGlnGluLeuAlaArgLeuGluThrProTyrTyrLeuValGly	200
QY	1243	CGGAGCCAGCTGAGGAGACAGCTCCGCGCAGAGTACAACTGACGAGCAGCAGCGAG	1302
Db	201	ArgArgProAlaGlyGlnSerSerGlyGlnSerAspAsnCysSerSerSerGlu	220
QY	1303	GCCAAAGCGGCGTGGAGCTGCTGGCGGCGGCTGCTGCGGCGCTACATCACC	1362
Db	221	AlaAsnGlyThrGlyLeuGluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThr	240
QY	1363	TCCTCTACTTCCACTGACAGCCTCACCAGCGTGGGCTTCGGCAACGTCCGCAAC	1422
Db	241	SerLeuTyrPheAlaLeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsn	260
QY	1423	ACGAGCAGCAGAGATCTTCTCATCTGCACCATGCTCATCGGCGGCTGATGCAGCG	1482
Db	261	ThrAspThrGluLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAla	280
QY	1483	GTGGTGTGGGACGTGAGCGGCATCATCCAGCGATGACCGCCGCTTCTGTGAC	1542
Db	281	ValValPheGlyAsnValThrAlaIleIleGlnArgMetTyrAlaArgPheLeuTyr	300
QY	1543	CACAGCGCAGCGGACCTGCGGACTATCATCGCATCCAGCTGATCCCAAGCCCTC	1602
Db	301	HisSerArgThrArgAspLeuArgAspTyrIleArgIleHisArgIleProLysProLeu	320
QY	1603	AAGCAGCGCATGCTGGAGTACTTCCAGCGCAGCTGGCGGTGACAAATGGCATGCAC	1662
Db	321	LysGlnArgMetLeuGluTyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThr	340
QY	1663	ACGAGTGTGTCAGACCTCCCTGAGAGCTGGCGCGCAGACATCGCCATGCCATCCAC	1722
Db	341	ThrGluLeuLeuGlnSerLeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHis	360
QY	1723	AAGAGTCTGTCAGCGCCACTGTTGAGCGCGCCAGCGGCTGCTCGCGGCACTG	1782
Db	361	LysGluValLeuGlnLeuProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeu	380
QY	1783	TCTGTGCGCTGCGCGCGCTTCTGCACGCGCGGCGAGTACCTCATCCACCAAGCGGAT	1842
Db	381	SerLeuAlaLeuArgProAlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAsp	400
QY	1843	GCCCTGAGCGCCTACTTGTCTGTGCTGGCTCCATGGAGGTGCTCAAGGTGGCACC	1902
Db	401	AlaLeuGlnAlaLeuTyrPheValCysSerGlySerMetGluValLeuLysGlyGlyThr	420
QY	1903	GTGCTGCGCATCCAGGAGCGGCACTGATCGGCTGTGAGCTGCCCGCGCGGAGCAG	1962
Db	421	ValLeuAlaIleLeuGlyLysGlyAspLeuIleGlyCysGluLeuProArgArgGluGln	440
QY	1963	GTGTAAGGCCAATGCGGAGTGNAGGGGTGAGTACTCGCTCCGCTCGAC	2013
Db	441	ValValLysAlaAsnAlaAspValLysGlyLeuThrTyrCysValLeuGln	457
DE	Drosophila melanogaster polypeptide SEQ ID NO 10494.		
XX	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.		
KW	Drosophila melanogaster.		
OS	WO200171042-A2.		
XX	27-SEP-2001.		
XX	23-MAR-2001; 2001WO-US09231.		
PF	23-MAR-2000; 2000US-191637P.		
XX	11-JUL-2000; 2000US-0614150.		
PR	(PEKE) PE CORP NY.		
XX	Venter JC, Adams M, Li PWD, Myers EW;		
PI	WPI: 2001-656860/75.		
XX	N-PSDB; ABL05337.		
DR	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions		
XX	Disclosure; SEQ ID NO 10494; 2lpp + Sequence Listing; English.		
PS	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).		
CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.		
XX	SQ Sequence 1311 AA;		
Alignment Scores:	1.69e-115 Length: 1311		
Pred. No.:	1901.00 Matches: 455		
Score:	53.85% Conservative: 146		
Percent Similarity:	40.77% Mismatches: 273		
Best Local Similarity:	31.22% Indels: 242		
Query Match:	22 Gaps: 31		
DB:	US-09-965-830-1_COPY_6_3257 (1-3252) x ABB61234 (1-1311)		
QY	1	ATGCGCGCCATCGCGGCTCCTGGCGCTCAGACACTCTCTGGACACCATCGTACG	60
Db	28	MetProAlaArgLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr	47
QY	61	CGCTTCGACGCGCACAGTAACCTGCTGTCGGCAACGCCAGGTGGCGGCTCTTC	120
Db	48	ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnAlaAsnGly---	Asn 66
QY	121	CCCCTGGTCTACTGCTGTGCTGTGTGCTACCTCAGCGGCTTCTCCCGGCTGAGTC	180
Db	67	ProIleValTyrCysSerAspGlyPheValAspLeuThrGlyTyrSerArgAlaGlnIle	86
QY	181	ATGACGCGGGCTGTGCTGCTCTCTCTCTTTATGGGCGACACACAGTGCCTCCGC	240
Db	87	MetGlnLysGlyCysSerCysHisPheLeuTyrGlyProAspThrLysGluGluHis	Lys 106
QY	241	CAACAGATCCGACAGGCGCTGGACGACAGGAGTTCACAGGCTGAGCTGATCTGTAC	300
Db	107	GlnGlnIleGluLysSerLeuSerAsnLysMetGluLeuLysLeuGluValIlePheTyr	126

[illegible][illegible]

chromosome 3p21.3-24.3.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 131 /note= "Encoded by ARA"

Misc-difference 151 /note= "Encoded by ARA"

Domain 226..247 /label= Transmembrane_domain

Domain 303..327 /label= Transmembrane_domain

Domain 354..377 /label= Transmembrane_domain

Domain 449..473 /label= Transmembrane_domain

Domain 423..442 /label= P_loop

WO200005346-A1.

03-FEB-2000.

21-JUL-1999; 99WO-US16752.

21-JUL-1998; 98US-O119855.

(MILL-) MILLENNIUM PHARM INC.

Curtis RAJ;

WPI; 2000-182682/16.

N-PSDB; NAZ50453.

Novel gene encoding potassium channel molecule useful in treating central nervous system disorders such as Alzheimer's disease, multiple sclerosis, and schizophrenia

Claim 9; Fig 2; 144pp; English.

The present sequence is a partial ERG-like protein 2 (ERG-LP2) which is a member of ERG potassium channel family. This sequence is a result of initial sequencing of clone jhbaa042h05 which was obtained from human brain library. ERG-LP2 gene is mapped to human chromosome 3p21.3-24.3, between markers WI-4218 and RP_L15_1. It is predominantly expressed in the brain.

The protein functions as a potassium channel modulator and has neuroprotective, antiparkinsonian, anticonvulsant, antidepressant, neuroleptic and nootropic activities. The present sequence is useful for treating several potassium channel mediated disorders (CNS disorders) such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, epilepsy, depression, schizophrenia and amnesia.

Sequence 542 AA;

Alignment Scores:

Pred. No.: 3 67e-111 Length: 542

Score: 1832.50 Matches: 351

Percent Similarity: 77.64% Conservative: 83

Best Local Similarity: 62.79% Indels: 33

Query Match: 30.10% Gaps: 5

DB:

US-09-965-830-1_COPY_6_3257 (1-3252) x AAY44905 (1-542)

QY 1 ATCCGGCGCATGGGGCCCTCTGGCCCTCAGAACACCTTCTTGAGACACATCGCTACG 60

Db 1 MetProValMetLysGlyLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

QY 61 CGCTTCAGCGCACGCCACGACACTTCTGTGTTGGCAACGCCCGGAGGTGGGCTCTTC 120

Db 21 ArgPheAspGlyThrHisSerAsnPhelleLeuAlaGlnValAlaLysGlyPhe 40

